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OM protein - protein search, using sw model

Run on: May 20, 2006, 20:15:01 ; Search time 84 Seconds
(without alignments)
789.243 Million cell updates/sec

Title: US-10-705-716a-2
Sequence: 1 MCGGGRADAIERYEYEW.....VTENIKOMDSKVTAKCIN 145

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A_Geneseq.8:*
1: geneseqp19808:*
2: geneseqp19908:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20048:*
8: geneseqp20058:*
9: geneseqp20068:*
10: geneseqp20078:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	767	100.0	145	8	ADO48473 Rat PTH r
2	746	97.3	145	8	ADO48479 Mouse PTH
3	645	84.1	145	4	AA895018 Human pro
4	645	84.1	145	5	AA019498 HSI prote
5	645	84.1	145	6	ABR58646 Human can
6	645	84.1	145	7	ADC31800 Human nov
7	645	84.1	145	8	ADM46959 Brain and
8	645	84.1	145	8	ADO48475 Human PTH
9	617.5	80.5	149	7	ADM46961 Brain and
10	473.5	61.7	149	7	ADM46963 Brain and
11	333.5	43.7	92	5	ADO81902 Human dlo
12	294	38.3	54	8	ADO48481 Mouse PTH
13	288	37.5	73	7	ADM46962 Brain and
14	278	36.2	54	7	ADM46960 Brain and
15	278	36.2	54	8	ADO48477 Human PTH
16	272	35.5	80	7	ADM46964 Brain and
17	140	18.3	25	7	ADM46979 Brain and
18	99	12.9	18	7	ADM46977 Brain and
19	92.5	12.1	778	2	AA13456 Duffy rec
20	89	11.6	16	8	ADO48482 PTH respo
21	87.5	11.4	260	4	ABG09889 Novel hum
22	87.5	11.4	592	4	ABG15607 Novel hum
23	85.5	11.1	274	8	ADY09773 Plant full

24	84	11.0	718	6	ABU17344
25	84	11.0	726	6	ADA36828
26	83.5	10.9	700	5	AAE25052
27	83	10.8	1433	5	ABP35624
28	82	10.7	339	6	AAE14866
29	81.5	10.6	600	7	ADJ70139
30	81.5	10.6	852	4	AAH40296
31	81.5	10.6	872	4	AAH40295
32	81.5	10.6	866	4	AAH42081
33	81.5	10.6	886	4	AAH42082
34	81.5	10.6	950	8	ADQ89824
35	81.5	10.6	974	4	AAU31506
36	80.5	10.5	275	4	ABG21379
37	80.5	10.5	275	4	ABG15431
38	80.5	10.5	320	8	ADX73952
39	80.5	10.5	1100	4	AAH4930
40	79.5	10.4	286	2	AAV00097
41	79.5	10.4	286	5	ABP43316
42	79.5	10.4	286	6	ABU88344
43	79.5	10.4	286	6	ABU13595
44	79.5	10.4	286	9	ADY38910
45	79.5	10.4	305	2	AAV00096

ALIGNMENTS

RESULT 1
ID ADO48473 standard; protein, 145 AA.
AC ADO48473;
XX
DT 12-AUG-2004 (first entry)
XX
DE Rat PTH responsive gene protein.
XX
KW PTH responsive gene; PARG; bone-forming; bone; bone density modulation;
KM transgenic animal; osteoporotic; gene therapy; osteoporosis; rat.
XX
OS Rattus sp.
XX
PN WO2004044152-A2.
XX
PD 27-MAY-2004.
XX
PF 10-NOV-2003; 2003WO-US035655.
XX
PR 12-NOV-2002; 2002US-0425532P.
XX
PA (AMHP) WYETH.
XX
PI Robinson JA, Stojanovic-Suenic V, Babij P, Murrills RJ,
XX WPI; 2004-420299/39.
XX N-PSDB; ADO48472.
XX
PT New nucleic acid fragment encoding a PARG polypeptide, useful in
PT preparing a composition for diagnosing, treating or preventing bone
PT related disorders, e.g., osteoporosis.
XX
PS Claim 9; SEQ ID NO 2; 169pp; English.
XX
CC The invention relates to a novel PTH responsive gene (PARG) fragment
CC encoding a polypeptide. The invention further comprises: a chimeric
CC construct comprising the isolated nucleic acid fragment operatively
CC linked to suitable regulatory sequences; a host cell transformed with the
CC chimeric construct; a vector comprising the nucleic acid fragment;
CC obtaining a nucleic acid fragment encoding the polypeptide; a method for
CC obtaining a polypeptide; detecting the presence of the nucleic acid
CC fragment; an antibody that specifically binds to one or more epitopes of
CC a PARG polypeptide; a composition for regulating bone-forming activity
CC in a mammal comprising the nucleic acid fragment, polypeptide or antibody

CC ; an agent that alters the expression of PABG gene or polypeptide;
CC determining whether an agent alters the expression of PABG mRNA;
CC screening agents for effectiveness in altering expression of the nucleic
CC acid fragment; screening for agents useful for treating bone related
CC disorders; evaluating the efficacy of a treatment of a bone related
CC disorder in a subject; identifying polypeptides capable of binding to
CC PABG; monitoring the effectiveness of treatment of a subject with a bone
CC related agent; a transgenic animal comprising the DNA, an animal model
CC for the study of bone density modulation comprising a first group of
CC animals composed of the transgenic animal and a second group of control
CC animals; studying bone mass determinants; studying the modulation of bone
CC mass; studying an effect of PABG on bone disorders; identifying an agent
CC for treating bone related disorders; identifying whether an agent which
CC has bone forming activity; and a stably transfected cell line comprising
CC two constructs, the first construct comprising a ligand binding domain
CC linked to a DNA binding domain which is linked to an activation domain
CC all of which expression is driven by a constitutive promoter, the second
CC construct comprising multiple copies of DNA binding elements linked to a
CC minimal promoter which is linked to PABG cDNA, where upon the addition
CC of chemical inducer, transcription of PABG gene is induced. The PABG
CC polynucleotide has osteopathic activity. The PTH responsive gene may be
CC used to treat disorders by gene therapy. The nucleic acid is useful in
CC preparing a composition for diagnosing, treating or preventing bone
CC related disorders, e.g., osteoporosis. This sequence represents a PTH
CC responsive gene protein of the invention.

XX Sequence 145 AA;

Query Match 100.0%; Score 767; DB 8; Length 145;

Best Local Similarity 100.0%; Pred. No. 4, 9e-76; Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCGGSRADAIERPRYESWTRETESTWLTITDSDALPSAAATDSGPEAGGLHAGVLEDP 60
DB 1 MCGGSRADAIERPRYESWTRETESTWLTITDSDALPSAAATDSGPEAGGLHAGVLEDP 60
QY 61 SSGVLRPAAPGGINPEKKKNCGTQCPNSQSLSSGPILOKONGLMTTEAKDKAKMSAR 120
DB 61 SSGVLRPAAPGGINPEKKKNCGTQCPNSQSLSSGPILOKONGLMTTEAKDKAKMSAR 120
QY 121 EVAISTENIRQMDRSKRVTKNCIN 145
DB 121 EVAISTENIRQMDRSKRVTKNCIN 145

RESULT 2

AD048479 standard; protein; 145 AA.

XX AD048479;

DT 12-AUG-2004 (first entry)

DE Mouse PTH responsive gene protein.

XX PTH responsive gene; PABG; bone-forming; bone; bone density modulation;
KM transgenic animal; osteopathic; gene therapy; osteoporosis; mouse;
KW murine.

XX Mus sp.

XX W0200404152-A2.

XX 27-MAY-2004.

XX 10-NOV-2003; 2003WC-US035655.

XX 12-NOV-2002; 2002US-0425532P.

XX (AMHP) WYETH.

XX Robinson JA, Stojanovic-Susulic V, Badij P, Murrills RJ;

DR MPI: 2004-420299/39.

DR N-PSDB; AD048478.

PT New nucleic acid fragment encoding a PABG polypeptide, useful in

PT preparing a composition for diagnosing, treating or preventing bone

PT related disorders, e.g., osteoporosis.

XX Claim 9; SEQ ID NO 8; 169pp; English.

XX The invention relates to a novel PTH responsive gene (PABG) fragment
CC encoding a polypeptide. The invention further comprises: a chimeric
CC construct comprising the isolated nucleic acid fragment operatively
CC linked to suitable regulatory sequences; a host cell transformed with the
CC chimeric construct; a vector comprising the nucleic acid fragment;
CC obtaining a nucleic acid fragment encoding the polypeptide; a method for
CC obtaining a polypeptide; detecting the presence of the nucleic acid
CC fragment; an antibody that specifically binds to one or more epitopes of
CC a PABG polypeptide; a composition for regulating bone-forming activity
CC in a mammal comprising the nucleic acid fragment, polypeptide or antibody
CC ; an agent that alters the expression of PABG gene or polypeptide;
CC determining whether an agent alters the expression of PABG mRNA;
CC screening agents for effectiveness in altering expression of the nucleic
CC acid fragment; screening for agents useful for treating bone related
CC disorders; evaluating the efficacy of a treatment of a bone related
CC disorder in a subject; identifying polypeptides capable of binding to
CC PABG; monitoring the effectiveness of treatment of a subject with a bone
CC related agent; a transgenic animal comprising the DNA, an animal model
CC for the study of bone density modulation comprising a first group of
CC animals composed of the transgenic animal and a second group of control
CC animals; studying bone mass determinants; studying the modulation of bone
CC mass; studying an effect of PABG on bone disorders; identifying an agent
CC for treating bone related disorders; identifying whether an agent which
CC has bone forming activity; and a stably transfected cell line comprising
CC two constructs, the first construct comprising a ligand binding domain
CC linked to a DNA binding domain which is linked to an activation domain
CC all of which expression is driven by a constitutive promoter, the second
CC construct comprising multiple copies of DNA binding elements linked to a
CC minimal promoter which is linked to PABG cDNA, where upon the addition
CC of chemical inducer, transcription of PABG gene is induced. The PABG
CC polynucleotide has osteopathic activity. The PTH responsive gene may be
CC used to treat disorders by gene therapy. The nucleic acid is useful in
CC preparing a composition for diagnosing, treating or preventing bone
CC related disorders, e.g., osteoporosis. This sequence represents a PTH
CC responsive gene protein of the invention.

XX Sequence 145 AA;

Query Match 97.3%; Score 746; DB 8; Length 145;

Best Local Similarity 97.2%; Pred. No. 1e-73; Matches 141; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MCGGSRADAIERPRYESWTRETESTWLTITDSDALPSAAATDSGPEAGGLHAGVLEDP 60
DB 1 MCGGSRADAIERPRYESWTRETESTWLTITDSDALPSAAATDSGPEAGGLHAGVLEDP 60
QY 61 SSGVLRPAAPGGINPEKKKNCGTQCPNSQSLSSGPILOKONGLMTTEAKDKAKMSAR 120
DB 61 SSGVLRPAAPGGINPEKKKNCGTQCPNSQSLSSGPILOKONGLMTTEAKDKAKMSAR 120
QY 121 EVAISTENIRQMDRSKRVTKNCIN 145
DB 121 EVAISTENIRQMDRSKRVTKNCIN 145

RESULT 3

AD048479 standard; protein; 145 AA.

XX AD048479;

DT 26-JUN-2001 (first entry)

XX Human protein sequence SEQ ID NO:16726.

XX KM Human; primer; detection; diagnosis; antisense therapy; gene therapy.
 XX OS Homo sapiens.
 XX PN EP1074617-A2.
 XX PD 07-FEB-2001.
 XX PF 28-JUL-2000; 2000EP-00116126.
 XX PR 29-JUL-1999; 99JP-00248036.
 XX PR 27-AUG-1999; 99JP-00300253.
 XX PR 11-JAN-2000; 2000JP-00118776.
 XX PR 02-MAY-2000; 2000JP-00183767.
 XX PR 09-JUN-2000; 2000JP-00241899.
 XX PA (HELI-) HELIX RES INST.
 XX PI Ota T, Isegai T, Nishikawa T, Hayaishi K, Saito K, Yamamoto J;
 XX PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX DR WPI; 2001-318749/34.
 XX PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-
 PT length cDNAs defined in the specification, and for the detection and/or
 PT diagnosis of the abnormality of the proteins encoded by the full-length
 PT cDNAs.
 XX PS Claim 8; SEQ ID NO 16726; 2537pp + Sequence listing; English.
 XX CC The present invention describes primer sets for synthesising 5602 full-
 CC length cDNAs defined in the specification. Where a primer set comprises:
 CC (a) an oligo-dT primer and an oligonucleotide complementary to the
 CC complementary strand of a polynucleotide which comprises one of the 5602
 CC nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in the
 CC specification. The primer sets can be used in antisense therapy and in
 CC gene therapy. The primers are useful for synthesising polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
 CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
 CC oligonucleotides, all of which are used in the exemplification of the
 CC present invention
 XX SQ Sequence 145 AA;
 XX
 QY Query Match 84.1%; Score 645; DB 4; Length 145;
 QY Best Local Similarity 83.4%; Pred. No. 1,4e-62;
 QY Matches 121; Conservative 10; Mismatches 14; Indels 0; Gaps 0;
 QY 1 MCGGGRADAIERPRYESTWRTREESTWLTYYTSDALPSAAATDSGPEAGGAGAGVLEDGP 60
 QY 1 MCGGGRADAIERPRYESTWRTREESTWLTYYTSDALPSAAATDSGPEAGGAGAGVLEDGP 60
 DB 1 MCGGGRADAIERPRYESTWRTREESTWLTYYTSDALPSAAATDSGPEAGGAGAGVLEDGP 60
 QY 61 SSGNGVRPAPAGGIANPEKKKNGCTCCPNSSGGLTOKONGLTWTEAKRDAKMSAR 120
 QY 61 SSGNGVRPAPAGGIANPEKKKNGCTCCPNSSGGLTOKONGLTWTEAKRDAKMSAR 120
 DB 61 PSNGVPRSTAPGGINPEKKKTCCTCCPNPSSGGLTOKONGLTWTEAKRDAKMPAK 120
 QY 121 EVAISVTENIRQMDRSKRVTKNCIN 145
 QY 121 EVAISVTENIRQMDRSKRVTKNCIN 145
 DB 121 EVTINVTDSIQMDRSKRVTKNCIN 145

RESULT 4
 ID AAO19498 standard; protein; 145 AA.
 XX AC AAO19498;
 XX AC AAO19498;
 XX DT 20-DEC-2002 (first entry)
 XX DE HSI protein variant.
 XX KM HSI; variant; cancer; tumour; ungine cluster; cytostatic; metastasis;
 KM BST; expressed sequence tag; colon cancer; stomach cancer; breast cancer;
 KM HSI69395; HSI127144; HS2; HSI12793; HS3.
 XX OS Unidentified.
 XX PN DEL10103694-AL.
 XX PD 01-AUG-2002.
 XX PF 26-JAN-2001; 2001DE-01003694.
 XX PF 26-JAN-2001; 2001DE-01003694.
 XX PR 26-JAN-2001; 2001DE-01003694.
 XX PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
 XX PI Bretz D, Kemmerer W;
 XX DR WPI; 2002-644836/70.
 XX DR N-PSDB; AAL50100.
 XX PT Diagnosis and therapy of tumors, by determining expression rates of
 PT specific expressed sequence tags of the ungine cluster, and subsequently
 PT blocking their expression.
 XX PS Claim 10; Page 5; 10pp; German.
 XX CC The present invention relates to the use of expressed sequence tags
 CC (ESTs), or variants, of the ungine cluster HSI69395 (HS1), HSI127144
 CC (HS2) and/or HSI12793 (HS3) for diagnosis and therapy of tumors, in
 CC which their expression rates in tumour cells and/or lymph nodes are
 CC determined. The EST sequences are useful as prognostic markers of
 CC survival of cancer patients (high levels of EST-related mRNA are
 CC associated with a poor prognosis, specifically correlated with
 CC development of metastases); and for diagnosis and/or therapy of solid
 CC tumours, particularly of colon, stomach and breast. The present sequence
 CC is a variant of the HSI protein shown in the exemplification of the
 CC invention
 XX SQ Sequence 145 AA;
 XX
 QY Query Match 84.1%; Score 645; DB 5; Length 145;
 QY Best Local Similarity 83.4%; Pred. No. 1,4e-62;
 QY Matches 121; Conservative 10; Mismatches 14; Indels 0; Gaps 0;
 QY 1 MCGGGRADAIERPRYESTWRTREESTWLTYYTSDALPSAAATDSGPEAGGAGAGVLEDGP 60
 QY 1 MCGGGRADAIERPRYESTWRTREESTWLTYYTSDALPSAAATDSGPEAGGAGAGVLEDGP 60
 DB 1 MCGGGRADAIERPRYESTWRTREESTWLTYYTSDALPSAAATDSGPEAGGAGAGVLEDGP 60
 QY 61 SSGNGVRPAPAGGIANPEKKKNGCTCCPNSSGGLTOKONGLTWTEAKRDAKMSAR 120
 QY 61 SSGNGVRPAPAGGIANPEKKKNGCTCCPNSSGGLTOKONGLTWTEAKRDAKMSAR 120
 DB 61 PSNGVPRSTAPGGINPEKKKTCCTCCPNPSSGGLTOKONGLTWTEAKRDAKMPAK 120
 QY 121 EVAISVTENIRQMDRSKRVTKNCIN 145
 QY 121 EVAISVTENIRQMDRSKRVTKNCIN 145
 DB 121 EVTINVTDSIQMDRSKRVTKNCIN 145
 RESULT 5
 ID ABR58646 standard; protein; 145 AA.
 XX AC ABR58646;
 XX AC ABR58646;

XX 09-JUL-2003 (first entry)
 XX Human cancer related protein SEQ ID NO:303.
 DE Human cancer related protein SEQ ID NO:303.
 XX Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
 KM heart disease; atherosclerosis; endometriosia.
 XX Homo sapiens.
 OS WO2003025138-A2.
 PN 27-MAR-2003.
 PD 17-SEP-2002; 2002MO-US029560.
 XX 17-SEP-2002; 2001US-0323469P.
 PR 20-SEP-2001; 2001US-0323887P.
 PR 13-NOV-2001; 2001US-0350666P.
 PR 08-FEB-2002; 2002US-0355145P.
 PR 08-FEB-2002; 2002US-0355257P.
 PR 12-APR-2002; 2002US-0372246P.
 XX (EOSB-) EOS BIOTECHNOLOGY INC.
 PA Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
 PI Zlotnick A;
 PI WPI; 2003-354600/33.
 DR N-PSDB; ACC72796.
 XX New genes that are up-regulated or down-regulated in cancers, useful as
 PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
 PT therapeutic targets for screening drugs for treating these diseases.
 XX Claim 12; Page 753; 767pp; English.
 XX The present invention describes an isolated nucleic acid molecule, which
 CC comprises the sequence of any of the genes that are up-regulated or down-
 CC regulated in specific cancers (e.g. about 1031 genes up-regulated in
 CC acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
 CC related gene nucleotide sequences which encode the proteins given in
 CC ABR58521 to ABR58709. Also described: (1) determining the presence or
 CC absence of a pathological cell in a patient; (2) an expression vector
 CC comprising a nucleic acid molecule described above; (3) a host cell
 CC comprising the vector; (4) an isolated polypeptide, which is encoded by
 CC the nucleic acid; (5) an antibody that specifically binds the polypeptide
 CC of (4); (6) specifically targeting a compound to a pathological cell in a
 CC patient by administering to the patient the antibody above; and (7) a
 CC drug screening assay. The nucleic acid is useful as diagnostic markers or
 CC therapeutic targets. In particular, the nucleic acid is useful for
 CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
 CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
 CC pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,
 CC atherosclerosis and endometriosia. The nucleic acid is also useful in
 CC drug screening, particularly for identifying agents for treating these
 CC pathologies
 XX
 SQ Sequence 145 AA:
 Query Match 84.1%; Score 645; DB 6; Length 145;
 Best Local Similarity 83.4%; Pred. No. 1.4e-62;
 Matches 121; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

DB 121 EVTINVTDSIQMDRSRRITKNCVN 145
 |||:::|||||:|||||:
 RESULT 6
 ADC31800
 ID ADC31800 standard; protein, 145 AA.
 XX
 AC ADC31800;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human novel polypeptide sequence, SEQ ID NO:1882.
 XX
 KM Human; diagnostic; drug screening; forensics; gene mapping;
 KM biodiversity assessment; Parkinson's disease; Alzheimer's disease;
 KM neurodegenerative diseases; anaemia; platelet disorder; wound; burns;
 KM ulcers; osteoporosis; autoimmune disease; cancer;
 KM molecular weight marker; food supplement; antiparkinsonian; nootropic;
 KM neuroprotective; antianemic; anticoagulant; thrombolytic; vulnerary;
 KM anticancer; osteopathic; immunosuppressive; antiinflammatory; cytostatic;
 KM gene therapy; chromosome 8.
 XX Homo sapiens.
 OS
 XX WO2003029271-A2.
 PN
 XX 10-APR-2003.
 PD 24-SEP-2002; 2002MO-US030474.
 PF 24-SEP-2002; 2001US-0324631P.
 PR 24-SEP-2001; 2001US-0324631P.
 XX (HYSE-) HYSEQ INC.
 PA Tang TY, Zhang J, Ren F, Xue AJ, Zhao QJ, Wang J, Wehrman T;
 PI Zhou P, Ghosh M, Wang D, Ma Y, Asundi V, Wang Z, Weng G;
 PI Haley-Vicente D, Drmanac RT;
 XX
 XX WPI; 2003-371981/35.
 DR N-PSDB; ADC30829.
 XX New polynucleotide and polypeptide useful for diagnosing, preventing or
 PT treating conditions such as neurodegenerative diseases, anemias, platelet
 PT disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
 PT cancer.
 XX Claim 20; SEQ ID NO 1882; 1185pp; English.
 XX The invention relates to 971 novel human cDNA sequences (ADC29919-
 CC ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The
 CC invention also relates to nucleic acid sequences over 99% identical with
 CC the novel human cDNAs. The invention additionally encompasses expression
 CC vectors and host cells comprising a nucleic acid of the invention; the
 CC recombinant production of a polypeptide of the invention; an antibody
 CC against a polypeptide of the invention; a method of detecting
 CC polynucleotides or polypeptides of the invention; and methods of
 CC identifying a compound which binds to a polypeptide of the invention. The
 CC invention further discloses methods of preventing, treating or
 CC ameliorating a medical condition; kits comprising polynucleotide probes
 CC and/or monoclonal antibodies for carrying out the methods of the
 CC invention; methods for the identification of compounds that modulate the
 CC expression or activity of the polynucleotide and/or polypeptide; and 767
 CC contig sequences corresponding to the cDNA sequences of the invention
 CC (ADC31861-ADC32627) and the polypeptides encoded by the contigs (ADC32628
 CC ADC33394). The nucleic acids and polypeptides of the invention are
 CC useful in diagnostics, drug screening, forensics, gene mapping, in the
 CC identification of mutations responsible for genetic disorders or other
 CC traits, for assessing biodiversity, and in producing many other types of
 CC data and products dependent on DNA and amino acid sequences. They are
 CC also used for treating diseases such as Parkinson's disease, Alzheimer's
 CC disease and other neurodegenerative diseases, anaemia, platelet
 CC disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or

CC cancer. The nucleic acids may also be used as hybridization probes or
CC primers, and in the recombinant production of a protein. The polypeptides
CC are also useful in generating antibodies, as molecular weight markers,
CC and as food supplements. The present sequence represents a specifically
CC claimed human polypeptide sequence of the invention. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 145 AA;

Query Match 84.1%; Score 645; DB 7; Length 145;
Best Local Similarity 83.4%; Pred. No. 1,4e-62;

Matches 121; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 1 MCGCGSRADAIERPYYESWTRTESWLTYYTSDALPSAAATDSCPEAGGHHAGVLEDGP 60
DB 1 MCGCGSRADAIERPYYESWTRTESWLTYYTSDALPSAAATDSCPEAGGHHAGVLEDGL 60
QY 61 SSGNVLPAPAGGIAPNEKKNCGTCCPNSSGSLTCKONGLWTTAKRDARKRSAR 120
DB 61 PSNGVPRSTAPGGIPNEKKTNCCTCCPNSSGSLTCKONGLQTTAKRDARKRMPAK 120
QY 121 EVAISVTENIRQMDRSKRVTKNCIN 145
DB 121 EVTINVTDSIQMDRSRRITKNCVN 145

RESULT 7

AD048475
ID AD048475 standard; protein; 145 AA.

AC AD046959;

DT 03-JUN-2004 (first entry)

DE Brain and Acute Leukemia, Cytoplasmic alternate protein #1.

XX acute myelogenous leukemia; gene expression; BALC;

KW chronic myelogenous leukemia; prostate cancer; Brain and Acute Leukemia;

KM Cytoplasmic; exon.

XX Homo sapiens.

OS Key Location/Qualifiers

FT Misc-difference 41 /note="encoded by GCS"

XX WO2003040347-A2.

XX 15-MAY-2003.

PF 12-NOV-2002; 2002WO-US036375.

PR 09-NOV-2001; 2001US-0348210P.

XX (OHIS) UNIV OHIO STATE RES FOUND.

XX Tanner SM, De la Chapell A;

XX WPI, 2003-441564/41.

XX N-PSDB; AD046951.

XX Characterizing acute or chronic myelogenous leukemia, or prostate cancer

XX in a patient comprises assaying for the overexpression of one or more

XX BALC transcripts in cells obtained from the patient.

XX Disclosure; SEQ ID NO 17; 78bp; English.

XX The invention relates to a method of characterizing acute myelogenous

XX leukemia (AML) in a patient by assaying for the overexpression of one or

XX more BALC transcripts in cells obtained from the patient, where an

XX overexpression indicates that the patient has an aggressive form of AML.

CC The methods, kits and probes are useful for characterizing acute or
CC chronic myelogenous leukemia, or prostate cancer. They are also useful
CC for detecting BALC overexpression. This sequence corresponds to a BALC
CC (Brain and Acute Leukemia, Cytoplasmic) protein encoded by an alternative
CC spliced RNA consisting of exons 1, 6 and 8.

XX Sequence 145 AA;

Query Match 84.1%; Score 645; DB 7; Length 145;
Best Local Similarity 83.4%; Pred. No. 1,4e-62;

Matches 121; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 1 MCGCGSRADAIERPYYESWTRTESWLTYYTSDALPSAAATDSCPEAGGHHAGVLEDGP 60
DB 1 MCGCGSRADAIERPYYESWTRTESWLTYYTSDALPSAAATDSCPEAGGHHAGVLEDGL 60
QY 61 SSGNVLPAPAGGIAPNEKKNCGTCCPNSSGSLTCKONGLWTTAKRDARKRSAR 120
DB 61 PSNGVPRSTAPGGIPNEKKTNCCTCCPNSSGSLTCKONGLQTTAKRDARKRMPAK 120
QY 121 EVAISVTENIRQMDRSKRVTKNCIN 145
DB 121 EVTINVTDSIQMDRSRRITKNCVN 145

RESULT 8

AD048475
ID AD048475 standard; protein; 145 AA.

AC AD048475;

DT 12-AUG-2004 (first entry)

DE Human PTH responsive gene protein.

XX PTH responsive gene; PABG, bone-forming; bone; bone density modulation;

KW transgenic animal; osteopathic; gene therapy; osteoporosis; human.

XX Homo sapiens.

XX WO2004044152-A2.

XX 27-MAY-2004.

PF 10-NOV-2003; 2003WO-US035655.

PR 12-NOV-2002; 2002US-0425532P.

XX (AMHP) WYETH.

XX Robinson JA, Stojanovic-Susulic V, Bablj P, Murrills RJ;

XX WPI, 2004-420289/39.

XX N-PSDB; AD048474.

XX New nucleic acid fragment encoding a PABG polypeptide; useful in

XX preparing a composition for diagnosing, treating or preventing bone

XX related disorders, e.g., osteoporosis.

XX Claim 9; SEQ ID NO 4; 169bp; English.

XX The invention relates to a novel PTH responsive gene (PABG) fragment

XX encoding a polypeptide. The invention further comprises a chimeric

XX construct comprising the isolated nucleic acid fragment operatively

XX linked to suitable regulatory sequences; a host cell transformed with the

XX chimeric construct; a vector comprising the nucleic acid fragment;

XX obtaining a nucleic acid fragment encoding the polypeptide; a method for

XX fragment; an antibody that specifically binds to one or more epitopes of

XX a PABG polypeptide; a composition for regulating bone-forming activity

XX in a mammal comprising the nucleic acid fragment, polypeptide or antibody

XX ; an agent that alters the expression of PABG gene or polypeptide;

XX determining whether an agent alters the expression of PABG mRNA;

CC screening agents for effectiveness in altering expression of the nucleic
 CC acid fragment; screening for agents useful for treating bone related
 CC disorder; evaluating the efficacy of a treatment of a bone related
 CC disorder in a subject; identifying polypeptides capable of binding to
 CC PAIGB; monitoring the effectiveness of treatment of a subject with a bone
 CC related agent; a transgene animal comprising the DNA; an animal model
 CC for the study of bone density modulation comprising a first group of
 CC animals composed of the transgenic animal and a second group of control
 CC animals; studying bone mass determinants; studying the modulation of bone
 CC mass; studying an effect of PAIGB on bone disorders; identifying an agent
 CC for treating bone related disorders; identifying whether an agent which
 CC has bone forming activity; and a stably transfected cell line comprising
 CC two constructs, the first construct comprising a ligand binding domain
 CC linked to a DNA binding domain which is linked to an activation domain
 CC all of which expression is driven by a constitutive promoter, the second
 CC construct comprising multiple copies of DNA binding elements linked to a
 CC minimal promoter which is linked to PAIGB cDNA, where upon the addition
 CC of chemical inducer, transcription of PAIGB gene is induced. The PAIGB
 CC polynucleotide has osteopontin activity. The PTH responsive gene may be
 CC used to treat disorder by gene therapy. The nucleic acid is useful in
 CC preparing a composition for diagnosis, treating or preventing bone
 CC related disorders, e.g., osteoporosis. This sequence represents a PTH
 CC responsive gene protein of the invention.

XX Sequence 145 AA;

Query Match Best Local Similarity 84.1%; Score 645; DB 8; Length 145;

Matches 121; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 1 MCGCGSRADAIERPYESWTRTESTWLTYYTSDALPSAAATDSGPEAGGLHAGLEDDP 60
 DB 1 MCGCGSRADAIERPYESWTRTESTWLTYYTSDAPPSAAAPDSGPEAGGLHAGLEDDG 60
 QY 61 SSGVLRPAPPGIANGKKNKNGCQCPNOSLSSGPTKONGLTTEAKRDKKRSAR 120
 DB 61 PSNGVPRSTAPGGIPNEKKTCTCCPNFOSLSSGPTKONGLTTEAKRDKKRPAPK 120
 QY 121 EVAISTENIRQMDRSKRVTKNCIN 145
 DB 121 EVTINVTDSIQMDRSRRTKNCIN 145

RESULT 9

ADM46961 ID ADM46961 standard; protein; 180 AA.

XX ADM46961;

AC 03-JUN-2004 (first entry)

DE Brain and Acute Leukemia, Cytoplasmic alternate protein #3.

XX acute myelogenous leukemia; gene expression; BAALC;

KW chronic myelogenous leukemia; prostate cancer; Brain and Acute Leukemia;

XX Cytoplasmic; exon.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 41 /note= "encoded by GCS"

XX WO2003040347-A2.

XX 15-MAY-2003.

XX 12-NOV-2002; 2002WO-US036375.

XX 09-NOV-2001; 2001US-0348210P.

XX (OHIS) UNIV OHIO STATE RES FOUND.

PI Tanner SM, De La Chapell A;
 XX WPI; 2003-441564/41.
 DR N-PSDB; ADM46963.
 XX
 PT Characterizing acute or chronic myelogenous leukemia, or prostate cancer
 PT in a patient comprises assaying for the overexpression of one or more
 PT BAALC transcripts in cells obtained from the patient.
 XX
 PS Disclosure; SEQ ID NO 19; 78pp; English.

CC The invention relates to a method of characterizing acute myelogenous
 CC leukemia (AML) in a patient by assaying for the overexpression of one or
 CC more BAALC transcripts in cells obtained from the patient, where an
 CC overexpression indicates that the patient has an aggressive form of AML.
 CC The methods, kits and probes are useful for characterizing acute or
 CC chronic myelogenous leukemia, or prostate cancer. They are also useful
 CC for detecting BAALC overexpression. This sequence corresponds to a BAALC
 CC (Brain and Acute Leukemia, Cytoplasmic) protein encoded by an alternative
 CC spliced RNA consisting of exons 1, 6 and 8.

XX Sequence 180 AA;

Query Match Best Local Similarity 80.5%; Score 617.5; DB 7; Length 180;

Matches 121; Conservative 10; Mismatches 14; Indels 35; Gaps 1;

QY 1 MCGCGSRADAIERPYESWTRTESTWLTYYTSDALPSAAATDSGPEAGGLHAGLEDDP 53
 DB 1 MCGCGSRADAIERPYESWTRTESTWLTYYTSDAPPSAAAPDSGPEAGGLHAGLEDDG 60
 QY 54 -----GLEDGPPSSNGVLRPAPPGIANGKKNKNGCQCPN 85
 DB 61 KIRAPTVSDEGLFSAKXKAPLAVPSHGWLLEDGLPSNGVPRSTAPGGIPNEKKTCTCET 120
 QY 86 QCPNOSLSSGPTKONGLTTEAKRDKKRSARVAISTENIRQMDRSKRVTKNCIN 145
 DB 121 QCPNOSLSSGPTKONGLTTEAKRDKKRPKEVTINVTDSIQMDRSRRTKNCIN 180

RESULT 10

ADM46963 ID ADM46963 standard; protein; 149 AA.

XX ADM46963;

AC 03-JUN-2004 (first entry)

DE Brain and Acute Leukemia, Cytoplasmic alternate protein #5.

XX acute myelogenous leukemia; gene expression; BAALC;

KW chronic myelogenous leukemia; prostate cancer; Brain and Acute Leukemia;

XX Cytoplasmic; exon.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 41 /note= "encoded by GCS"

XX WO2003040347-A2.

XX 15-MAY-2003.

XX 12-NOV-2002; 2002WO-US036375.

XX 09-NOV-2001; 2001US-0348210P.

XX (OHIS) UNIV OHIO STATE RES FOUND.

XX Tanner SM, De La Chapell A;
 WPI; 2003-441564/41.

DR N-PSDB; ADM46955.
XX
XX Characterizing acute or chronic myelogenous leukemia, or prostate cancer
PT in a patient comprises assaying for the overexpression of one or more
PT BAML2 transcripts in cells obtained from the patient.
XX
XX Disclousure; SEQ ID NO 21; 78bp; English.
XX
XX The invention relates to a method of characterizing acute myelogenous
CC leukemia (AML) in a patient by assaying for the overexpression of one or
CC more BAML2 transcripts in cells obtained from the patient, where an
CC overexpression indicates that the patient has an aggressive form of AML.
CC The methods, kits and probes are useful for characterizing acute or
CC chronic myelogenous leukemia, or prostate cancer. They are also useful
CC for detecting BAML2 overexpression. This sequence corresponds to a BAML2
CC (Brain and Acute Leukemia, Cytoplasmic) protein encoded by an alternative
CC spliced RNA consisting of exons 1, 6 and 8.
XX
XX Sequence 149 AA;
SQ
Query Match 61.7%; Score 473.5; DB 7; Length 149;
Best Local Similarity 66.0%; Pred. No. 1.2e-43;
Matches 95; Conservative 2; Mismatches 12; Indels 35; Gaps 1;
QY 1 MGCGSRADALEPRYESTWETESTWLTYYDSALPSAAATDSPEAGLHA----- 53
DB 1 MGCGSRADALEPRYESTWETESTWLTYYDSALPSAAATDSPEAGLHVAEAKS 60
QY 54 -----GVLEDPSSNGVLRPAAPGGIAPNEKKMNCCT 85
DB 61 KIXAPTDSVSDGLEFSASKMAPLAVFSGHMLEDLPSNGVPRSTAPGAIPEKKTNCET 120
QY 86 QCPNSQSLSSGPTLTKONGLMWTE 109
DB 121 QCPNPQSLSSGPTLTKONGLOTTE 144
RESULT 11
ADQ81902
ID ADQ81902 standard; protein; 92 AA.
XX
XX ADQ81902;
AC
XX
XX 09-SEP-2004 (first entry)
DT
XX
XX Human dihydrogenase 10.12.
DE
XX
XX Human; enzyme; dihydrogenase 10.12; malignant tumour; inflammation;
KW immunological disease; haemopathy; HIV infection.
XX
XX Homo sapiens.
OS
XX
XX CN1344798-A.
PN
XX
XX 17-APR-2002.
PD
XX
XX 29-SEP-2000; 2000CN-00125495.
PF
XX
XX 29-SEP-2000; 2000CN-00125495.
PR
XX
XX (SHAN-) SHANGHAI BIODOR GENE DEV CO LTD.
QA
XX
XX Mao Y, Xie Y;
PI
XX
XX WPI; 2002-509506/55.
DR
XX
XX N-PSDB; ADQ81901.
XX
XX New polypeptide human dihydrogenase 10.12 and polynucleotides encoding this
PT polypeptide, useful for treating various diseases, such as malignant
PT tumor, inflammations, immunological diseases, hemopathy and HIV
PT infection.
XX
XX Claim 1; SEQ ID NO 2; 33pp; Chinese.

XX
XX The present invention discloses a new kind of polypeptide, human
CC dihydrogenase 10.12, polynucleotides encoding this polypeptide, a DNA
CC recombination process to produce the polypeptide and antagonist against
CC the polypeptide. The present invention also discloses the method of
CC applying the polypeptide in treating various diseases, such as malignant
CC tumors, inflammations, immunological diseases, hemopathy and HIV
CC infection. The present sequence is the human dihydrogenase 10.12.
XX
XX Sequence 92 AA;
SQ
Query Match 43.7%; Score 335.5; DB 5; Length 92;
Best Local Similarity 72.7%; Pred. No. 1.1e-28;
Matches 64; Conservative 9; Mismatches 10; Indels 5; Gaps 1;
QY 58 DGPSNGVLRPAAPGGIAPNEKKMNCCTQCPNSQSLSSGPTLTKONGLMWTEAKRDARM 117
DB 10 DGPEYGN-----APCGIPNEPKTNCETQCPNPQSLSSGPTLTKONGLOTTEAKRDARM 64
QY 118 SAREVAISVTENIRQMDRSKRVYTCIN 145
DB 65 PAKETVITWVDSIQMDRSRRITTCVN 92
RESULT 12
ADQ48481
ID ADQ48481 standard; protein; 54 AA.
XX
XX ADQ48481;
AC
XX
XX 12-AUG-2004 (first entry)
DT
XX
XX Mouse PTH responsive gene protein exon 2 splice variant.
DE
XX
XX PTH responsive gene; PARG; bone-forming; bone; bone density modulation;
KW transgenic animal; osteopathic; gene therapy; osteoporosis; mouse;
KW murine.
XX
XX Mus sp.
OS
XX
XX WO2004044152-A2.
PN
XX
XX 27-MAY-2004.
PD
XX
XX 10-NOV-2003; 2003WO-US035655.
PF
XX
XX 12-NOV-2002; 2002US-0425532P.
PR
XX
XX (AMHP) WYETH.
QA
XX
XX Robinson JA, Stojanovic-Susulic V, Babić P, Murrills RJ;
PI
XX
XX WPI; 2004-420299/39.
DR
XX
XX N-PSDB; ADQ48480.
XX
XX New nucleic acid fragment encoding a PARG polypeptide, useful in
PT preparing a composition for diagnosing, treating or preventing bone
PT related disorders, e.g., osteoporosis.
XX
XX Claim 9; SEQ ID NO 10; 169pp; English.
XX
XX The invention relates to a novel PTH responsive gene (PARG) fragment
CC encoding a polypeptide. The invention further comprises: a chimeric
CC construct comprising the isolated nucleic acid fragment operatively
CC linked to suitable regulatory sequences; a host cell transformed with the
CC chimeric construct; a vector comprising the nucleic acid fragment;
CC obtaining a nucleic acid fragment encoding the polypeptide; a method for
CC obtaining a polypeptide; detecting the presence of the nucleic acid
CC fragment; an antibody that specifically binds to one or more epitopes of
CC a PARG polypeptide; a composition for regulating bone-forming activity
CC in a mammal comprising the nucleic acid fragment, polypeptide or antibody
CC ; an agent that alters the expression of PARG gene or polypeptide;
CC determining whether an agent alters the expression of PARG mRNA;

screening agents for effectiveness in altering expression of the nucleic acid fragment; screening for agents useful for treating bone related disorders; evaluating the efficacy of a treatment of a bone related disorder in a subject; identifying polypeptides capable of binding to PAIGB; monitoring the effectiveness of treatment of a subject with a bone related agent; a transgenic animal comprising the DNA, an animal model for the study of bone density modulation comprising a first group of animals composed of the transgenic animal and a second group of control animals; studying bone mass determinants; studying the modulation of bone mass; studying an effect of PAIGB on bone disorders; identifying an agent for treating bone related disorders; identifying whether an agent which has bone forming activity, and a stably transfected cell line comprising two constructs, the first construct comprising a ligand binding domain linked to a DNA binding domain which is linked to an activation domain all of which expression is driven by a constitutive promoter, the second construct comprising multiple copies of DNA binding elements linked to a minimal promoter which is linked to PAIGB cDNA, where upon the addition of chemical inducer, transcription of PAIGB gene is induced. The PAIGB polynucleotide has osteopathic activity. The PTH responsive gene may be used to treat disorders by gene therapy. The nucleic acid is useful in preparing a composition for diagnosing, treating or preventing bone related disorders, e.g., osteoporosis. This sequence represents a PTH responsive gene protein of the invention.

Sequence 54 AA;

Query Match 38.3%; Score 294; DB 8; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.9e-24;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MCGCGSRADAIIEPRYESTRETSTWLTYSDALPSAAATDGGPAGGLHAG 54
1 MCGCGSRADAIIEPRYESTRETSTWLTYSDALPSAAATDGGPAGGLHAG 54

RESULT 13
ADM46962
ID ADM46962 standard; protein; 73 AA.
XX
XX ADM46962;
XX
XX 03-JUN-2004 (first entry)
XX
XX Brain and Acute Leukemia, Cytoplasmic alternate protein #4.
XX
XX acute myelogenous leukemia; gene expression; BAALC;
XX chronic myelogenous leukemia; prostate cancer; Brain and Acute Leukemia;
XX Cytoplasmic; exon.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Misc-difference 41 /note= "encoded by GCS"
XX
XX WO2003040347-A2.
XX
XX 15-MAY-2003.
XX
XX 12-NOV-2002; 2002MO-US036375.
XX
XX 09-NOV-2001; 2001US-0348210P.
XX
XX (OHIS) UNIV OHIO STATE RES FOUND.
XX
XX
XX Tanner SM, De La Chapell A;
XX
XX WPI; 2003-441564/41.
XX DR N-PSDB; ADM46954.
XX
XX Characterizing acute or chronic myelogenous leukemia, or prostate cancer
XX in a patient comprises assaying for the overexpression of one or more
XX BAALC transcripts in cells obtained from the patient.

XX
XX Disclosure; SEQ ID NO 20; 78pp; English.
XX
XX The invention relates to a method of characterizing acute myelogenous
XX leukemia (AML) in a patient by assaying for the overexpression of one or
XX more BAALC transcripts in cells obtained from the patient, where an
XX overexpression indicates that the patient has an aggressive form of AML.
XX The methods, kits and probes are useful for characterizing acute or
XX chronic myelogenous leukemia, or prostate cancer. They are also useful
XX for detecting BAALC overexpression. This sequence corresponds to a BAALC
XX (Brain and Acute Leukemia, Cytoplasmic) protein encoded by an alternative
XX spliced RNA consisting of exons 1, 6 and 8.

Sequence 73 AA;

Query Match 37.5%; Score 288; DB 7; Length 73;
Best Local Similarity 91.4%; Pred. No. 1.3e-23;
Matches 53; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

1 MCGCGSRADAIIEPRYESTRETSTWLTYSDALPSAAATDGGPAGGLHAG 58
1 MCGCGSRADAIIEPRYESTRETSTWLTYSDALPSAAATDGGPAGGLHAG 58

RESULT 14
ADM46960
ID ADM46960 standard; protein; 54 AA.
XX
XX ADM46960;
XX
XX 03-JUN-2004 (first entry)
XX
XX Brain and Acute Leukemia, Cytoplasmic alternate protein #2.
XX
XX acute myelogenous leukemia; gene expression; BAALC;
XX chronic myelogenous leukemia; prostate cancer; Brain and Acute Leukemia;
XX Cytoplasmic; exon.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Misc-difference 41 /note= "encoded by GCS"
XX
XX WO2003040347-A2.
XX
XX 15-MAY-2003.
XX
XX 12-NOV-2002; 2002MO-US036375.
XX
XX 09-NOV-2001; 2001US-0348210P.
XX
XX (OHIS) UNIV OHIO STATE RES FOUND.
XX
XX
XX Tanner SM, De La Chapell A;
XX
XX WPI; 2003-441564/41.
XX DR N-PSDB; ADM46952.
XX
XX Characterizing acute or chronic myelogenous leukemia, or prostate cancer
XX in a patient comprises assaying for the overexpression of one or more
XX BAALC transcripts in cells obtained from the patient.

Disclosure; SEQ ID NO 18; 78pp; English.

The invention relates to a method of characterizing acute myelogenous
leukemia (AML) in a patient by assaying for the overexpression of one or
more BAALC transcripts in cells obtained from the patient, where an
overexpression indicates that the patient has an aggressive form of AML.
The methods, kits and probes are useful for characterizing acute or
chronic myelogenous leukemia, or prostate cancer. They are also useful
for detecting BAALC overexpression. This sequence corresponds to a BAALC
(Brain and Acute Leukemia, Cytoplasmic) protein encoded by an alternative

CC spliced RNA consisting of exons 1, 6 and 8.
 XX Sequence 54 AA;
 SQ

Query Match 36.2%; Score 278; DB 7; Length 54;
 Best Local Similarity 94.4%; Pred. No. 1.1e-22;
 Matches 51; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MCGCGSRADAIEPRYBSWTRETESTWLTYYTDSALPSAAATDSGPAGGIIHAG 54
 Db 1 MCGCGSRADAIEPRYBSWTRETESTWLTYYTDSALPSAAATDSGPAGGIIHAG 54

RESULT 15
 ADO48477
 ID ADO48477 standard; protein, 54 AA.
 XX ADO48477;
 AC
 XX 12-AUG-2004 (first entry)
 DT
 XX Human PTH responsive gene protein exon 2 splice variant.
 DE
 XX PTH responsive gene; PARGB; bone-forming; bone; bone density modulation;
 KM transgenic animal; osteopathic; gene therapy; osteoporosis; human.
 XX
 OS Homo sapiens.
 OS
 XX MO2004044152-A2.
 PN
 XX 27-MAY-2004.
 PD
 XX 10-NOV-2003; 2003MO-US035655.
 PF
 XX 12-NOV-2002; 2002US-0425532P.
 PR
 XX (AMHP) WYETH.
 PA
 XX Robinson JA, Stojanovic-Susulic V, Babij P, Murrills RJ;
 PI
 XX WPI; 2004-420299/39.
 DR N-PSDB; ADO48476.
 DR
 XX New nucleic acid fragment encoding a PARGB polypeptide, useful in
 PT preparing a composition for diagnosing, treating or preventing bone
 PT related disorders, e.g., osteoporosis.
 XX
 XX Claim 9; SEQ ID NO 6; 169pp; English.
 PS
 XX The invention relates to a novel PTH responsive gene (PARGB) fragment
 CC encoding a polypeptide. The invention further comprises: a chimeric
 CC construct comprising the isolated nucleic acid fragment operatively
 CC linked to suitable regulatory sequences; a host cell transformed with the
 CC chimeric construct; a vector comprising the nucleic acid fragment;
 CC obtaining a nucleic acid fragment encoding the polypeptide; a method for
 CC obtaining a polypeptide; detecting the presence of the nucleic acid
 CC fragment; an antibody that specifically binds to one or more epitopes of
 CC a PARGB polypeptide; a composition for regulating bone-forming activity
 CC in a mammal comprising the nucleic acid fragment, polypeptide or antibody
 CC ; an agent that alters the expression of PARGB gene or polypeptide;
 CC determining whether an agent alters the expression of PARGB mRNA;
 CC screening agents for effectiveness in altering expression of the nucleic
 CC acid fragment; screening for agents useful for treating bone related
 CC disorders; evaluating the efficacy of a treatment of a bone related
 CC disorder in a subject; identifying polypeptides capable of binding to
 CC PARGB; monitoring the effectiveness of treatment of a subject with a bone
 CC related agent; a transgenic animal comprising the DNA; an animal model
 CC for the study of bone density modulation comprising a first group of
 CC animals composed of the transgenic animal and a second group of control
 CC animals; studying bone mass determinants; studying the modulation of bone
 CC mass; studying an effect of PARGB on bone disorders; identifying an agent
 CC for treating bone related disorders; identifying whether an agent which
 CC has bone forming activity; and a stably transfected cell line comprising

CC two constructs, the first construct comprising a ligand binding domain
 CC linked to a DNA binding domain which is linked to an activation domain
 CC all of which expression is driven by a constitutive promoter, the second
 CC construct comprising multiple copies of DNA binding elements linked to a
 CC minimal promoter which is linked to PARGB cDNA, where upon the addition
 CC of chemical inducer, transcription of PARGB gene is induced. The PARGB
 CC polynucleotide has osteopathic activity. The PTH responsive gene may be
 CC used to treat disorders by gene therapy. The nucleic acid is useful in
 CC preparing a composition for diagnosing, treating or preventing bone
 CC related disorders, e.g., osteoporosis. This sequence represents a PTH
 CC responsive gene protein of the invention.

XX Sequence 54 AA;
 SQ

Query Match 36.2%; Score 278; DB 8; Length 54;
 Best Local Similarity 94.4%; Pred. No. 1.1e-22;
 Matches 51; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MCGCGSRADAIEPRYBSWTRETESTWLTYYTDSALPSAAATDSGPAGGIIHAG 54
 Db 1 MCGCGSRADAIEPRYBSWTRETESTWLTYYTDSALPSAAATDSGPAGGIIHAG 54

Search completed: May 20, 2006, 20:18:06
 Job time : 86 secs

SEQ ID NO:4:
LENGTH: 778
5198347-4

Query Match 12.1%; Score 92.5; DB 7; Length 778;
Best Local Similarity 33.0%; Pred. No. 0.14;
Matches 29; Conservative 12; Mismatches 44; Indels 3; Gaps 3;

QY 31 TDSALPSAATDSGPEAGLHAGVLEDPSSNGV-LRPAAGGIANPEKMC-GTQCP 88
DB 352 TVSDVDSVGGKDGSGSTASHALAGENGHNHGTDTPEKDEKADPOKDIYVKGQDT 411

QY 89 NSQSLS-GLPTOKONGLWTEAKRDAK 115
DB 412 DDRSGSLGPHYDERATLGETHMEKDT 439

RESULT 3

US-09-328-352-8115
Sequence 8115, Application US/09328352
Patent No. 6562958

GENERAL INFORMATION:

APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328.352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 8115
LENGTH: 726
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-8115

Query Match 11.0%; Score 84; DB 2; Length 726;
Best Local Similarity 35.1%; Pred. No. 1.2; Indels 20; Gaps 4;
Matches 27; Conservative 8; Mismatches 22

QY 2 GCGSRDAIEPRYESTETETWTYTSDALPSA--AATDSC-----PEAGLHAG 54
DB 181 GFGAGREVWPDVDVWNGDEKE--WLAHRSEALAGSNLAATENGILYVNP----- 231

QY 55 VLBDPSSNGVLRPAAP 71
DB 232 ----GPGASGDPFSAAP 244

RESULT 4

US-09-408-647A-2
Sequence 2, Application US/09408647A
Patent No. 6399858

GENERAL INFORMATION:

APPLICANT: Kobayashi, Donald
TITLE OF INVENTION: Chitinase Gene from Stenotrophomonas
FILE REFERENCE: Rut-Cook 98-0090
CURRENT APPLICATION NUMBER: US/09/408.647A
CURRENT FILING DATE: 1999-08-26
PRIOR APPLICATION NUMBER: 60/098.036
PRIOR FILING DATE: 1998-08-27
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 700
TYPE: PRT
ORGANISM: Stenotrophomonas maltophilia

FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1) ... (41)
NAME/KEY: DOMAIN
LOCATION: (196) ... (290)
NAME/KEY: DOMAIN

LOCATION: (330) ... (483)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank No. 6399858 AF014950
DATABASE ENTRY DATE: 1997-09-23
US-09-408-647A-2

Query Match 10.9%; Score 83.5; DB 2; Length 700;
Best Local Similarity 24.0%; Pred. No. 1.4;
Matches 31; Conservative 14; Mismatches 57; Indels 27; Gaps 2;

QY 26 TWLTYTSDALPSAATDSGPEAGLHAGVLEDPSSNGVLRPAAGGIANPEKMC----- 81
DB 159 TWANASGSHTFKAVATDNNNAVTSSATVSVTYASNDTTPSPVPGGLSPSKATVTN 218

QY 82 -----NCG-----TQCPNSQSLSGPLTOKONGLWTEAKRDAKMS 118
DB 219 LVMSAATDNGSGGVAGYDYVRNGSLVSPSATQYTDGGLTASTAYTYTARADNAGNAS 278

QY 119 AREVAISVT 127
DB 279 AQSGSISVT 287

RESULT 5

US-09-487-558B-60
Sequence 60, Application US/09487558B
Patent No. 6943356

GENERAL INFORMATION:

APPLICANT: Busby, Robert
APPLICANT: Cali, Brian
APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin
APPLICANT: Maxon, Mary
APPLICANT: Milne, Todd
APPLICANT: Royer, John
APPLICANT: Salama, Sofie
APPLICANT: Sherman, Amir
APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.130
CURRENT APPLICATION NUMBER: US/09/487.558B
CURRENT FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/487.558
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 446
SOFTWARE: PatentIn version 3.0
SEQ ID NO 60
LENGTH: 1433
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-09-487-558B-60

Query Match 10.8%; Score 83; DB 2; Length 1433;
Best Local Similarity 29.4%; Pred. No. 4.4;
Matches 32; Conservative 15; Mismatches 50; Indels 12; Gaps 4;

QY 36 LPSAATDSGPEAGLHAGVLEDPSSNGVLRPAAGGIANPEKMC-GTQCPNSQSLS 95
DB 927 LPPATTTSLKPLDGSQSKSLNKRQTPVYK-----ENPEHEIYXGDSNNNNSEA 979

QY 96 G--PLTOKONGLWTEAKRDAKMSAREVAISVTENIR--QMDRSKVT 140
DB 980 GHSPTWTNTGNKRLKYEKDAKR--NAKDGISKGENAHNFONDTKKMS 1027

RESULT 6

US-09-071-035-176
Sequence 176, Application US/09071035
Patent No. 6448043

GENERAL INFORMATION:

APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brooks
REGISTRATION NUMBER: PB369P2
REFERENCE/DOCKET NUMBER: PB369P2
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 176:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-071-035-176

Query Match 10.4%; Score 79.5; DB 2; Length 286;
Best Local Similarity 26.6%; Pred. No. 1.1;
Matches 47; Conservative 16; Mismatches 73; Indels 41; Gaps 9;

QY 3 CGG-----SRDAIEPRYSW---TRETSTWLTYSDDLPSAAT-DGSPBAG 49
DB 1 CGGKSTENDSRSSAESTVSTKASATKSSK-ATTKSDAKSGTTTADSKATAS 59
QY 50' GLHAGVLEDGSSNGVLRPAAPGGIANPEKKM-CGTQCPN---SQSLSSGPLTKOKNGL 105
DB 60 STKEA-----ANNSSAEKOSPANANPDQANQVLNQLANMFGQGLPAAILTSQTNF 113
QY 106 WTEAKRDARKMARBAIVSTENIRQMD-RSKRYT-----KNCIN 145
DB 114 LTAATTSQADQNNFRVLYAEKAIIPVNDARVNLTPISSEFKKTYGSDAEAKNAV 170

RESULT 7
US-10-206-576-176
Sequence 176, Application US/10206576
Patent No. 6913907
GENERAL INFORMATION:
APPLICANT: Choi et al.
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 497
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: Dell Latitude

OPERATING SYSTEM: Windows 98
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/206,576
FILING DATE: 29-Jul-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/071,035
FILING DATE: 1998-05-04
APPLICATION NUMBER: US 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: US 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: US 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
NAME: Hyman, Mark J.
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB369P1D1
INFORMATION FOR SEQ ID NO: 176:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 176:
US-10-206-576-176

Query Match 10.4%; Score 79.5; DB 2; Length 286;
Best Local Similarity 26.6%; Pred. No. 1.1;
Matches 47; Conservative 16; Mismatches 73; Indels 41; Gaps 9;

QY 3 CGG-----SRDAIEPRYSW---TRETSTWLTYSDDLPSAAT-DGSPBAG 49
DB 1 CGGKSTENDSRSSAESTVSTKASATKSSK-ATTKSDAKSGTTTADSKATAS 59
QY 50' GLHAGVLEDGSSNGVLRPAAPGGIANPEKKM-CGTQCPN---SQSLSSGPLTKOKNGL 105
DB 60 STKEA-----ANNSSAEKOSPANANPDQANQVLNQLANMFGQGLPAAILTSQTNF 113
QY 106 WTEAKRDARKMARBAIVSTENIRQMD-RSKRYT-----KNCIN 145
DB 114 LTAATTSQADQNNFRVLYAEKAIIPVNDARVNLTPISSEFKKTYGSDAEAKNAV 170

RESULT 8
US-09-071-035-174
Sequence 174, Application US/09071035
Patent No. 6448043
GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB369P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 174:
SEQUENCE CHARACTERISTICS:
LENGTH: 305 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-071-035-174

Query Match 10.4%; Score 79.5; DB 2; Length 305;
Best Local Similarity 26.6%; Pred. No. 1.2;
Matches 47; Conservative 16; Mismatches 73; Indels 41; Gaps 9;

QY 3 CGG-----SRADAEPRYTESW---TRTESTWLTYSDDLPSAAT-DSGEAG 49
DB 20 CGGKSTENTDSRSAAESTTVESTKASATKSSK-ATTSSDAKSGTTADSKATAS 78
QY 50 GLHAGVLEDPSSNGVLRPAAPGGIANPEKKN-CGTQCPN---SGLSSGPTLQKONGL 105
DB 79 STKEA-----ANGSABKQSPAKNANPDDQANQVNLNMFPGGLPAAILTSQTNNF 132
QY 106 WTEAKRDAKMSAREVAISVTENIRQMD-RSKRVT-----KXCIN 145
DB 133 LTAATTSQADQNNFRVLYAEKEAIPVNDARVNLTPISSEFKKTYGSDAEAKNANV 189

RESULT 9
US-10-206-576-174
Sequence 174, Application US/10206576
Patent No. 6913907
GENERAL INFORMATION:
APPLICANT: Choi et al.
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 497
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: Dell latitude
OPERATING SYSTEM: Windows 98
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/206,576
FILING DATE: 29-Jul-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/071,035
FILING DATE: 1998-05-04
APPLICATION NUMBER: US 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: US 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: US 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
NAME: Hyman, Mark J.
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB369P1D1
INFORMATION FOR SEQ ID NO: 174:
SEQUENCE CHARACTERISTICS:
LENGTH: 305 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 174:
US-10-206-576-174

Query Match 10.4%; Score 79.5; DB 2; Length 305;
Best Local Similarity 26.6%; Pred. No. 1.2;
Matches 47; Conservative 16; Mismatches 73; Indels 41; Gaps 9;

QY 3 CGG-----SRADAEPRYTESW---TRTESTWLTYSDDLPSAAT-DSGEAG 49
DB 20 CGGKSTENTDSRSAAESTTVESTKASATKSSK-ATTSSDAKSGTTADSKATAS 78
QY 50 GLHAGVLEDPSSNGVLRPAAPGGIANPEKKN-CGTQCPN---SGLSSGPTLQKONGL 105
DB 79 STKEA-----ANGSABKQSPAKNANPDDQANQVNLNMFPGGLPAAILTSQTNNF 132
QY 106 WTEAKRDAKMSAREVAISVTENIRQMD-RSKRVT-----KXCIN 145
DB 133 LTAATTSQADQNNFRVLYAEKEAIPVNDARVNLTPISSEFKKTYGSDAEAKNANV 189

RESULT 10
US-10-076-622-552
Sequence 552, Application US/10076622
Patent No. 6958361
GENERAL INFORMATION:
APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: PERSING, David H.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.470C11
CURRENT APPLICATION NUMBER: US/10/076,622
CURRENT FILING DATE: 2002-02-13
NUMBER OF SEQ ID NOS: 627
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 552
LENGTH: 661
TYPE: PRF
ORGANISM: Homo sapiens
US-10-076-622-552

Query Match 10.4%; Score 79.5; DB 2; Length 661;
Best Local Similarity 21.5%; Pred. No. 3.6;
Matches 37; Conservative 28; Mismatches 58; Indels 49; Gaps 7;

QY 7 RADAIAP-----RYESWTRTESTWLTYSDDLPSAATDSGPAGGLHAGVLEDP 60
DB 401 RADBIIPSESKQDVESWSLCEVQKQVCPKAHOKKEIDKIN-----GKLESP 456
QY 61 SSNGVLRPAAPGGIANPEKKN-----NCGTQCPNS 90
DB 457 DNGGFLKSPCRMVSLPTKALBLMDQTFKAEPEKPSAFEPALIMOKSVNKLAKNE 516
QY 91 QSLSSG---PLTQKONGL-----WTEAKRDAKMSAREVAISVTENIRQMDR 135
DB 517 QTLRADQMPSEBSKQKNVENSWSDESIRLT--VSQKDVCPKATYHKKENDX 566

RESULT 11
US-10-124-805-552
Sequence 552, Application US/10124805
Patent No. 6969518
GENERAL INFORMATION:
APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R.
APPLICANT: Persing, David H.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.470C12

;; CURRENT APPLICATION NUMBER: US/10/124,805
;; CURRENT FILING DATE: 2002-04-15
;; NUMBER OF SEQ ID NOS: 627
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 552
;; LENGTH: 661
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-124-805-552

Query Match 10.4%; Score 79.5; DB 2; Length 661;
Best Local Similarity 21.5%; Pred. No. 3.6;
Matches 37; Conservative 28; Mismatches 58; Indels 49; Gaps 7;

QY 7 RADAIER-----RYESWTRETESTWLTYYTDS-ALPSAATDSGPAGLHAGVLEDP 60
DB 401 RADILPSESKQDYESSWDSLSLCTVSQKVCPLPKAHQKEIDKIN---GKLEESP 456
QY 61 SSNGVLRPAAPGIANPEKQ-----NCGTQCPNS 90
DB 457 DNDGFLKSPCRMVSIPTKALELMDQTFKAPPEKPSAFEPALEMOKSVPNKALEKNE 516
QY 91 QSLSSG---PLTKQKNGL-----WTTAKRDAKMSAREVAISVTENIRQMDR 135
DB 517 QTLRADQMPSESKQKQNVENSWSLSLRET--VSQKDVCPKATKQKEMDK 566

RESULT 12
US-10-076-622-553
; Sequence 553, Application US/10076622
; Patent No. 6958361
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.470C11
; CURRENT APPLICATION NUMBER: US/10/076,622
; CURRENT FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 553
; LENGTH: 1013
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-076-622-553

Query Match 10.4%; Score 79.5; DB 2; Length 1013;
Best Local Similarity 21.5%; Pred. No. 6.7;
Matches 37; Conservative 28; Mismatches 58; Indels 49; Gaps 7;

QY 7 RADAIER-----RYESWTRETESTWLTYYTDS-ALPSAATDSGPAGLHAGVLEDP 60
DB 401 RADILPSESKQDYESSWDSLSLCTVSQKVCPLPKAHQKEIDKIN---GKLEESP 456
QY 61 SSNGVLRPAAPGIANPEKQ-----NCGTQCPNS 90
DB 457 DNDGFLKSPCRMVSIPTKALELMDQTFKAPPEKPSAFEPALEMOKSVPNKALEKNE 516
QY 91 QSLSSG---PLTKQKNGL-----WTTAKRDAKMSAREVAISVTENIRQMDR 135
DB 517 QTLRADQMPSESKQKQNVENSWSLSLRET--VSQKDVCPKATKQKEMDK 566

RESULT 13
US-10-124-805-553
; Sequence 553, Application US/10124805
; Patent No. 6969518
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Persing, David H.

;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;; FILE REFERENCE: 210121.470C12
;; CURRENT APPLICATION NUMBER: US/10/124,805
;; CURRENT FILING DATE: 2002-04-15
;; NUMBER OF SEQ ID NOS: 627
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 553
;; LENGTH: 1013
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-124-805-553

Query Match 10.4%; Score 79.5; DB 2; Length 1013;
Best Local Similarity 21.5%; Pred. No. 6.7;
Matches 37; Conservative 28; Mismatches 58; Indels 49; Gaps 7;

QY 7 RADAIER-----RYESWTRETESTWLTYYTDS-ALPSAATDSGPAGLHAGVLEDP 60
DB 401 RADILPSESKQDYESSWDSLSLCTVSQKVCPLPKAHQKEIDKIN---GKLEESP 456
QY 61 SSNGVLRPAAPGIANPEKQ-----NCGTQCPNS 90
DB 457 DNDGFLKSPCRMVSIPTKALELMDQTFKAPPEKPSAFEPALEMOKSVPNKALEKNE 516
QY 91 QSLSSG---PLTKQKNGL-----WTTAKRDAKMSAREVAISVTENIRQMDR 135
DB 517 QTLRADQMPSESKQKQNVENSWSLSLRET--VSQKDVCPKATKQKEMDK 566

RESULT 14
US-08-374-077C-2
; Sequence 2, Application US/08374077C
; Patent No. 6027912
; GENERAL INFORMATION:
; APPLICANT: Hall, Linda M.
; APPLICANT: Ren, Dejian
; APPLICANT: Zheng, Wei
; APPLICANT: Dubald, Manuel Marcel Paul
; TITLE OF INVENTION: Genes Encoding an Invertebrate Alpha1
; TITLE OF INVENTION: Calcium Channel Subunit
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHEIS, LLP
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/374,077C
; FILING DATE: 19-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm M.
; REGISTRATION NUMBER: 39,300
; REFERENCE/DOCKET NUMBER: 022650-264
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2516 amino acids
; TYPE: amino acid
; TOPOLOGY: 1linear
; MOLECULE TYPE: protein
US-08-374-077C-2

Query Match 10.2%; Score 78.5; DB 2; length 2516;
 Best Local Similarity 22.4%; Pred. No. 33;
 Matches 39; Conservative 21; Mismatches 61; Indels 53; Gaps 8;
 QY 3 CGGSRADAIERY--YESWTFETESTWLTITDSDALPSAAATDGPAGGILHAGVLEDGP 60
 DB 207 CGGGGIGAPPPRLTPPEAMQLOPQ-----NSVTSAGSTSSFSGG-----GR 249
 QY 61 SSNGVLPAAPGIANPEKKNK-----GTQC-----PNS 90
 DB 250 DNNSSY--SAVGGSSSSNSCNCITGTGNSLHGLGVGDVCSFTIADCDNSEDDDGDPNN 307
 QY 91 QSLSSGPL-TOKONGIATTEAKRDARMSAREVAISVTENIRQMRKRYTKNC 143
 DB 308 QDLSSTGLRTAIVAAVAAAKKQAEQSLADCE-SFSDRRQDADEPVRITIQDC 360

QY 91 QSLSSGPL-TOKONGIATTEAKRDARMSAREVAISVTENIRQMRKRYTKNC 143
 DB 308 QDLSSTGLRTAIVAAVAAAKKQAEQSLADCE-SFSDRRQDADEPVRITIQDC 360
 Search completed: May 20, 2006, 21:21:21
 Job time : 52 secs

RESULT 15
 US-08-895-590-2
 ; Sequence 2, Application US/08895590
 ; Patent No. 6207410
 ; GENERAL INFORMATION:
 ; APPLICANT: Hall, Linda M.
 ; APPLICANT: Ren, Dejian
 ; APPLICANT: Zheng, Wei
 ; APPLICANT: Dubald, Manuel Marcel Paul
 ; TITLE OF INVENTION: Genes Encoding an Insect Calcium Channel
 ; NUMBER OF SEQUENCES: 101
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
 ; STREET: 699 Prince Street
 ; CITY: Alexandria
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22314-3187
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/895,590
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/374,888
 ; FILING DATE: 19-JAN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: McGowan, Malcolm M.
 ; REGISTRATION NUMBER: 39,300
 ; REFERENCE/DOCKET NUMBER: 022650-263
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703-836-6620
 ; TELEFAX: 703-836-2021
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2516 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-895-590-2

Query Match 10.2%; Score 78.5; DB 2; length 2516;
 Best Local Similarity 22.4%; Pred. No. 33;
 Matches 39; Conservative 21; Mismatches 61; Indels 53; Gaps 8;

QY 3 CGGSRADAIERY--YESWTFETESTWLTITDSDALPSAAATDGPAGGILHAGVLEDGP 60
 DB 207 CGGGGIGAPPPRLTPPEAMQLOPQ-----NSVTSAGSTSSFSGG-----GR 249
 QY 61 SSNGVLPAAPGIANPEKKNK-----GTQC-----PNS 90
 DB 250 DNNSSY--SAVGGSSSSNSCNCITGTGNSLHGLGVGDVCSFTIADCDNSEDDDGDPNN 307

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OM protein - protein search, using sw model

Run on: May 20, 2006, 21:21:43 ; Search time 74 Seconds

(without alignments)
907.651 Million cell updates/sec

Title: US-10-705-716A-2

Perfect score: 1 MCGGSRADAIPEPRYTESWT.....VTENIRQMDRSKRVTKNCIN 145

Sequence: BLOSUM62

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:*
1: /EMC_Celerra_SIDS3/prodata/2/pubppa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/prodata/2/pubppa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/prodata/2/pubppa/US09_PUBCOMB.pep:*
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5: /EMC_Celerra_SIDS3/prodata/2/pubppa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/prodata/2/pubppa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	ID	Description
1	767	100.0	145	US-10-705-716A-2	Sequence 2, Appl1
2	746	97.3	145	US-10-705-716A-8	Sequence 8, Appl1
3	645	84.1	145	US-10-293-239-17	Sequence 17, Appl1
4	645	84.1	145	US-10-177-390-30	Sequence 30, Appl1
5	645	84.1	145	US-10-705-716A-4	Sequence 4, Appl1
6	617.5	80.5	180	US-10-293-239-19	Sequence 19, Appl1
7	473.5	61.7	149	US-10-293-239-21	Sequence 21, Appl1
8	294	38.3	54	US-10-705-716A-10	Sequence 10, Appl1
9	288	37.5	73	US-10-293-239-20	Sequence 20, Appl1
10	278	36.2	54	US-10-293-239-18	Sequence 18, Appl1
11	272	35.5	80	US-10-705-716A-6	Sequence 6, Appl1
12	272	35.5	80	US-10-293-239-22	Sequence 22, Appl1
13	140	18.3	25	US-10-293-239-37	Sequence 37, Appl1
14	99	12.9	18	US-10-293-239-35	Sequence 35, Appl1
15	94	12.3	147	US-10-767-701-48905	Sequence 48905, A
16	93	12.1	394	US-10-425-115-236244	Sequence 236244, A
17	89	11.6	16	US-10-705-716A-11	Sequence 11, Appl1
18	87.5	11.4	260	US-10-450-763-40258	Sequence 40258, A
19	87.5	11.4	592	US-10-450-763-45965	Sequence 45965, A
20	85.5	11.1	264	US-10-425-115-275422	Sequence 275422, A
21	85.5	11.1	274	US-10-425-114-65588	Sequence 65588, A
22	85	11.0	450	US-10-437-963-137075	Sequence 137075, A
23	84	11.0	718	US-10-282-122A-45268	Sequence 45268, A
24	83	10.8	1433	US-09-801-368-60	Sequence 60, Appl1
25	83	10.8	1433	US-10-149-310-112	Sequence 112, Appl1
26	82.5	10.8	514	US-11-188-298-18211	Sequence 18211, A
27	82.5	10.8	539	US-10-424-599-227399	Sequence 227399, A

28	82.5	10.8	609	US-10-437-963-144983	Sequence 144983, A
29	82	10.7	339	US-10-494-495-9	Sequence 9, Appl1
30	82	10.7	1491	US-10-437-963-140197	Sequence 140197, A
31	82	10.7	1597	US-10-437-963-180225	Sequence 180225, A
32	81.5	10.6	600	US-10-408-765A-1945	Sequence 1945, Appl1
33	81.5	10.6	950	US-10-745-237-254	Sequence 254, Appl1
34	81	10.6	670	US-10-156-761-14107	Sequence 14107, A
35	80.5	10.5	275	US-10-450-763-45790	Sequence 45790, A
36	80.5	10.5	275	US-10-450-763-51738	Sequence 51738, A
37	80.5	10.5	330	US-10-425-114-43318	Sequence 43318, A
38	80.5	10.5	508	US-10-437-963-188141	Sequence 188141, A
39	79.5	10.4	286	US-09-071-035-176	Sequence 176, Appl1
40	79.5	10.4	286	US-10-206-576-176	Sequence 176, Appl1
41	79.5	10.4	286	US-10-912-362-174	Sequence 174, Appl1
42	79.5	10.4	305	US-09-071-035-174	Sequence 174, Appl1
43	79.5	10.4	305	US-10-206-576-174	Sequence 174, Appl1
44	79.5	10.4	305	US-10-912-362-174	Sequence 174, Appl1
45	79.5	10.4	661	US-10-007-805-552	Sequence 552, Appl1

ALIGNMENTS

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RESULT 1
US-10-705-716A-2
; Sequence 2, Application US/10705716A
; Publication No. US20040146906A1
; GENERAL INFORMATION:
; APPLICANT: Robinson, John Allen
; APPLICANT: Stojanovic-Suenilic, Vedrana
; APPLICANT: Babji, Philip
; TITLE OF INVENTION: A Novel PTH Responsive Gene
; FILE REFERENCE: AM100401
; CURRENT APPLICATION NUMBER: US/10/705, 716A
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: US 60/425, 532
; PRIOR FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Rat
; US-10-705-716A-2

Query Match      100.0%; Score 767; DB 4; Length 145;
Best Local Similarity 100.0%; Pred. No. 5.4e-69;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MCGGSRADAIPEPRYTESWTRETESTWLTYSDDALPSAAATDSCGEAGIHAQVLEDPG 60
      1 MCGGSRADAIPEPRYTESWTRETESTWLTYSDDALPSAAATDSCGEAGIHAQVLEDPG 60
DB      1 MCGGSRADAIPEPRYTESWTRETESTWLTYSDDALPSAAATDSCGEAGIHAQVLEDPG 60
QY      61 SNGVLRPAAPGIANPEKKNCGTQCPNSQSISGSPLTQKNGLTWTTAKDQAKMSAR 120
      61 SNGVLRPAAPGIANPEKKNCGTQCPNSQSISGSPLTQKNGLTWTTAKDQAKMSAR 120
DB      61 SNGVLRPAAPGIANPEKKNCGTQCPNSQSISGSPLTQKNGLTWTTAKDQAKMSAR 120
QY      121 EVAISTENIRQMDRSKRVTKNCIN 145
      121 EVAISTENIRQMDRSKRVTKNCIN 145
DB      121 EVAISTENIRQMDRSKRVTKNCIN 145
QY      121 EVAISTENIRQMDRSKRVTKNCIN 145
      121 EVAISTENIRQMDRSKRVTKNCIN 145
DB      121 EVAISTENIRQMDRSKRVTKNCIN 145
RESULT 2
US-10-705-716A-8
; Sequence 8, Application US/10705716A
; Publication No. US20040146906A1
; GENERAL INFORMATION:
; APPLICANT: Robinson, John Allen
; APPLICANT: Stojanovic-Suenilic, Vedrana
; APPLICANT: Babji, Philip
; APPLICANT: Murrills, Richard John
; TITLE OF INVENTION: A Novel PTH Responsive Gene
```

FILE REFERENCE: AM100401
CURRENT APPLICATION NUMBER: US/10/705, 716A
CURRENT FILING DATE: 2003-11-10
PRIOR APPLICATION NUMBER: US 60/425,532
PRIOR FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn version 3.2
SEQ ID NO 8
LENGTH: 145
TYPE: PRT
ORGANISM: Mouse
US-10-705-716A-8

Query Match 97.3%; Score 746; DB 4; Length 145;
Best Local Similarity 97.2%; Pred. No. 7.1e-67;
Matches 141; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MCGGSRADAIIPRYESWTRETSTWLTYYTSDALPSAAATDSGPBAGGLHAGVLEDCP 60
DB 1 MCGGSRADAIIPRYESWTRETSTWLTYYTSDALPSAAATDSGPBAGGLHAGVLEDCG 60
QY 61 SSNGVLPPAPAGGIANPEKKNCGTCCPNSSQSLSSGGLTQKONGLWTEAKRDAKMSAR 120
DB 61 SSNGVLPPAPAGGIANPEKKNCGTCCPNSSQSLSSGGLTQKONGLWTEAKRDAKMSAR 120
QY 121 EVAISTENIRQMDRSKRVTKNCIN 145
DB 121 EVAISTENIRQMDRSKRVTKNCIN 145

RESULT 3
US-10-293-239-17
Sequence 17, Application US/10293239
Publication No. US20030119043A1
GENERAL INFORMATION:
APPLICANT: Tanner, Stephan
TITLE OF INVENTION: BALC expression as a diagnostic marker for acute leukemia
FILE REFERENCE: 22727/04101
CURRENT APPLICATION NUMBER: US/10/293,239
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: US 60/348,210
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO 17
LENGTH: 145
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-239-17

Query Match 84.1%; Score 645; DB 4; Length 145;
Best Local Similarity 83.4%; Pred. No. 1e-56;
Matches 121; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 1 MCGGSRADAIIPRYESWTRETSTWLTYYTSDALPSAAATDSGPBAGGLHAGVLEDCP 60
DB 1 MCGGSRADAIIPRYESWTRETSTWLTYYTSDALPSAAATDSGPBAGGLHAGVLEDCG 60
QY 61 SSNGVLPPAPAGGIANPEKKNCGTCCPNSSQSLSSGGLTQKONGLWTEAKRDAKMSAR 120
DB 61 PSNGVPRSTAPPGIIPNEKKTNCETCCPNSSQSLSSGGLTQKONGLWTEAKRDAKMPAK 120
QY 121 EVAISTENIRQMDRSKRVTKNCIN 145
DB 121 EVAISTENIRQMDRSKRVTKNCIN 145

RESULT 4
US-10-177-390-30
Sequence 30, Application US/10177390
Publication No. US20030143743A1
GENERAL INFORMATION:

APPLICANT: Schuler, Gerold
APPLICANT: N.V. Antwerp Innovatiecentrum
TITLE OF INVENTION: Improved transfection of Eucaryotic Cells with Linear
TITLE OF INVENTION: Polynucleotides by Electroporation
FILE REFERENCE: 021505wo/JH/ml
CURRENT APPLICATION NUMBER: US/10/177,390
CURRENT FILING DATE: 2002-06-20
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 30
LENGTH: 145
TYPE: PRT
ORGANISM: Homo sapiens
US-10-177-390-30

Query Match 84.1%; Score 645; DB 4; Length 145;
Best Local Similarity 83.4%; Pred. No. 1e-56;
Matches 121; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 1 MCGGSRADAIIPRYESWTRETSTWLTYYTSDALPSAAATDSGPBAGGLHAGVLEDCP 60
DB 1 MCGGSRADAIIPRYESWTRETSTWLTYYTSDALPSAAATDSGPBAGGLHAGVLEDCG 60
QY 61 SSNGVLPPAPAGGIANPEKKNCGTCCPNSSQSLSSGGLTQKONGLWTEAKRDAKMSAR 120
DB 61 PSNGVPRSTAPPGIIPNEKKTNCETCCPNSSQSLSSGGLTQKONGLWTEAKRDAKMPAK 120
QY 121 EVAISTENIRQMDRSKRVTKNCIN 145
DB 121 EVAISTENIRQMDRSKRVTKNCIN 145

RESULT 5
US-10-705-716A-4
Sequence 4, Application US/10705716A
Publication No. US20040146906A1
GENERAL INFORMATION:
APPLICANT: Robinson, John Allen
APPLICANT: Stojanovic-Suenllic, Vedrana
APPLICANT: Bablj, Philip
APPLICANT: Murrille, Richard John
TITLE OF INVENTION: A Novel PTH Responsive Gene
FILE REFERENCE: AM100401
CURRENT APPLICATION NUMBER: US/10/705, 716A
CURRENT FILING DATE: 2003-11-10
PRIOR APPLICATION NUMBER: US 60/425,532
PRIOR FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4
LENGTH: 145
TYPE: PRT
ORGANISM: Homo sapiens
US-10-705-716A-4

Query Match 84.1%; Score 645; DB 4; Length 145;
Best Local Similarity 83.4%; Pred. No. 1e-56;
Matches 121; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 1 MCGGSRADAIIPRYESWTRETSTWLTYYTSDALPSAAATDSGPBAGGLHAGVLEDCP 60
DB 1 MCGGSRADAIIPRYESWTRETSTWLTYYTSDALPSAAATDSGPBAGGLHAGVLEDCG 60
QY 61 SSNGVLPPAPAGGIANPEKKNCGTCCPNSSQSLSSGGLTQKONGLWTEAKRDAKMSAR 120
DB 61 PSNGVPRSTAPPGIIPNEKKTNCETCCPNSSQSLSSGGLTQKONGLWTEAKRDAKMPAK 120
QY 121 EVAISTENIRQMDRSKRVTKNCIN 145
DB 121 EVAISTENIRQMDRSKRVTKNCIN 145

RESULT 6

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us-10-293-239-19
; Sequence 19, Application US/10293239
; Publication No. US20030119043A1
; GENERAL INFORMATION:
; APPLICANT: Tanner, Stephan
; APPLICANT: de la Chapelle, Albert
; TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia
; FILE REFERENCE: 22727/04101
; CURRENT APPLICATION NUMBER: US/10/293,239
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 60/348,210
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 180
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-293-239-19
```

```
Query Match      80.5%; Score 617.5; DB 4; Length 180;
Best Local Similarity 67.2%; Pred. No. 8.1e-54;
Matches 121; Conservative 10; Mismatches 14; Indels 35; Gaps 1;
```

```
QY 1 MCGGSRADAIERPRYESWTRETSTWLTITDSDALPSAATDGPAGGILHA-----53
DB 1 MCGGSRADAIERPRYESWTRETSTWLTITDSDAPSAAPDGPAGGILHSLAEKS 60
QY 54 -----GVLEDPSSNGVLRPAAPGGINPEKKNCGT 85
DB 61 KIKAPDVSDEGLFSASKKAPLAVFSHGMLIEDGLPSNGVFRSTAPGGINPEKKNCGT 120
QY 86 QCPNSQSLSSGPILOKONGIMTTEAKDKARMSAREVAISVTENIRQWDSKRYTKNCIN 145
DB 121 QCPNPSLSSGPILOKONGILOTEAKDKARMPAKETVINTVDSIQWDSRRTTKNCVN 180
```

RESULT 7

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US-10-293-239-21
; Sequence 21, Application US/10293239
; Publication No. US20030119043A1
; GENERAL INFORMATION:
; APPLICANT: Tanner, Stephan
; APPLICANT: de la Chapelle, Albert
; TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia
; FILE REFERENCE: 22727/04101
; CURRENT APPLICATION NUMBER: US/10/293,239
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 60/348,210
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 149
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-293-239-21
```

```
Query Match      61.7%; Score 473.5; DB 4; Length 149;
```

```
Best Local Similarity 66.0%; Pred. No. 2e-39; Indels 35; Gaps 1;
```

```
QY 1 MCGGSRADAIERPRYESWTRETSTWLTITDSDALPSAATDGPAGGILHA-----53
DB 1 MCGGSRADAIERPRYESWTRETSTWLTITDSDAPSAAPDGPAGGILHSLAEKS 60
QY 54 -----GVLEDPSSNGVLRPAAPGGINPEKKNCGT 85
DB 61 KIKAPDVSDEGLFSASKKAPLAVFSHGMLIEDGLPSNGVFRSTAPGGINPEKKNCGT 120
QY 86 QCPNSQSLSSGPILOKONGIMTTE 109
DB 121 QCPNPSLSSGPILOKONGILOTE 144
```

```
RESULT 8
US-10-705-716A-10
; Sequence 10, Application US/10705716A
; Publication No. US20040146906A1
; GENERAL INFORMATION:
; APPLICANT: Robinson, John Allen
; APPLICANT: Stojanovic-Susulic, Vedrana
; APPLICANT: Babilj, Philip
; APPLICANT: Murrills, Richard John
; TITLE OF INVENTION: A Novel PTH Responsive Gene
; FILE REFERENCE: AM100401
; CURRENT APPLICATION NUMBER: US/10/705,716A
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: US 60/425,532
; PRIOR FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 54
; TYPE: PR1
; ORGANISM: Mouse
US-10-705-716A-10
```

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Query Match      38.3%; Score 294; DB 4; Length 54;
Best Local Similarity 100.0%; Pred. No. 6.6e-22;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 MCGGSRADAIERPRYESWTRETSTWLTITDSDALPSAATDGPAGGILHAG 54
DB 1 MCGGSRADAIERPRYESWTRETSTWLTITDSDALPSAATDGPAGGILHAG 54
```

RESULT 9

```
US-10-293-239-20
; Sequence 20, Application US/10293239
; Publication No. US20030119043A1
; GENERAL INFORMATION:
; APPLICANT: Tanner, Stephan
; APPLICANT: de la Chapelle, Albert
; TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia
; FILE REFERENCE: 22727/04101
; CURRENT APPLICATION NUMBER: US/10/293,239
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 60/348,210
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 73
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-293-239-20
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```
Query Match      37.5%; Score 288; DB 4; Length 73;
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```
Best Local Similarity 91.4%; Pred. No. 3.9e-21;
Matches 53; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
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```
QY 1 MCGGSRADAIERPRYESWTRETSTWLTITDSDALPSAATDGPAGGILHAGVLEID 58
DB 1 MCGGSRADAIERPRYESWTRETSTWLTITDSDAPSAAPDGPAGGILHSLAEKS 58
```

RESULT 10

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US-10-293-239-18
; Sequence 18, Application US/10293239
; Publication No. US20030119043A1
; GENERAL INFORMATION:
; APPLICANT: Tanner, Stephan
; APPLICANT: de la Chapelle, Albert
; TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia
; FILE REFERENCE: 22727/04101
```

;; CURRENT APPLICATION NUMBER: US/10/293,239
;; CURRENT FILING DATE: 2002-11-12
;; PRIOR APPLICATION NUMBER: US 60/348,210
;; PRIOR FILING DATE: 2001-11-09
;; NUMBER OF SEQ ID NOS: 39
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 18
;; LENGTH: 54
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-293-239-18

Query Match 36.2%; Score 278; DB 4; Length 54;
Best Local Similarity 94.4%; Pred. No. 2,7e-20;
Matches 51; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MCGGSRADAIERPRYSWTRETESTWLTITDSDALPSAAATDGGPAGGILHAG 54
Db 1 MCGGSRADAIERPRYSWTRETESTWLTITDSDALPSAAAPDGGPAGGILHSG 54

RESULT 11
US-10-705-716a-6
;; Sequence 6, Application US/10705716A
;; Publication No. US20040146906A1
;; GENERAL INFORMATION:
;; APPLICANT: Robinson, John Allen
;; APPLICANT: Stojanovic-Svulic, Vedrana
;; APPLICANT: Babil, Philip
;; APPLICANT: Murrills, Richard John
;; TITLE OF INVENTION: A Novel PTH Responsive Gene
;; FILE REFERENCE: AM100401
;; CURRENT APPLICATION NUMBER: US/10/705,716A
;; CURRENT FILING DATE: 2003-11-10
;; PRIOR APPLICATION NUMBER: US 60/425,532
;; PRIOR FILING DATE: 2002-11-12
;; NUMBER OF SEQ ID NOS: 63
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 6
;; LENGTH: 54
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-705-716a-6

Query Match 36.2%; Score 278; DB 4; Length 54;
Best Local Similarity 94.4%; Pred. No. 2,7e-20;
Matches 51; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MCGGSRADAIERPRYSWTRETESTWLTITDSDALPSAAATDGGPAGGILHAG 54
Db 1 MCGGSRADAIERPRYSWTRETESTWLTITDSDALPSAAAPDGGPAGGILHSG 54

RESULT 12
US-10-293-239-22
;; Sequence 22, Application US/10293239
;; Publication No. US20030119043A1
;; GENERAL INFORMATION:
;; APPLICANT: Tanner, Stephen
;; APPLICANT: de la Chapelle, Albert
;; TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia
;; FILE REFERENCE: 22727/04101
;; CURRENT APPLICATION NUMBER: US/10/293,239
;; CURRENT FILING DATE: 2002-11-12
;; PRIOR APPLICATION NUMBER: US 60/348,210
;; PRIOR FILING DATE: 2001-11-09
;; NUMBER OF SEQ ID NOS: 39
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 22
;; LENGTH: 80
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-293-239-22

Query Match 35.5%; Score 272; DB 4; Length 80;
Best Local Similarity 94.3%; Pred. No. 1,8e-19;
Matches 50; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MCGGSRADAIERPRYSWTRETESTWLTITDSDALPSAAATDGGPAGGILHAG 53
Db 1 MCGGSRADAIERPRYSWTRETESTWLTITDSDALPSAAAPDGGPAGGILHSG 53

RESULT 13
US-10-293-239-37
;; Sequence 37, Application US/10293239
;; Publication No. US20030119043A1
;; GENERAL INFORMATION:
;; APPLICANT: Tanner, Stephen
;; APPLICANT: de la Chapelle, Albert
;; TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia
;; FILE REFERENCE: 22727/04101
;; CURRENT APPLICATION NUMBER: US/10/293,239
;; CURRENT FILING DATE: 2002-11-12
;; PRIOR APPLICATION NUMBER: US 60/348,210
;; PRIOR FILING DATE: 2001-11-09
;; NUMBER OF SEQ ID NOS: 39
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 37
;; LENGTH: 25
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-293-239-37

Query Match 18.3%; Score 140; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 8e-07;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RADAIERPRYSWTRETESTWLTIT 31
Db 1 RADAIERPRYSWTRETESTWLTIT 25

RESULT 14
US-10-293-239-35
;; Sequence 35, Application US/10293239
;; Publication No. US20030119043A1
;; GENERAL INFORMATION:
;; APPLICANT: Tanner, Stephen
;; APPLICANT: de la Chapelle, Albert
;; TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia
;; FILE REFERENCE: 22727/04101
;; CURRENT APPLICATION NUMBER: US/10/293,239
;; CURRENT FILING DATE: 2002-11-12
;; PRIOR APPLICATION NUMBER: US 60/348,210
;; PRIOR FILING DATE: 2001-11-09
;; NUMBER OF SEQ ID NOS: 39
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 35
;; LENGTH: 18
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-293-239-35

Query Match 12.9%; Score 99; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0071;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DATEPRYSWTRETEST 26
Db 1 DATEPRYSWTRETEST 18

RESULT 15
US-10-767-701-48905
;; Sequence 48905, Application US/10767701

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; Publication No. US2004017268A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5353)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 48905
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3476-020-P1-K1-A12.pep
US-10-767-701-48905

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```

Query Match      12.3%; Score 94; DB 4; Length 147;
Best Local Similarity 27.5%; Pred. No. 0.32;
Matches 30; Conservative 17; Mismatches 52; Indels 10; Gaps 3;

```

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QY 36 LPSAAATDSGPEAGLHAGVLEDPSSNGVLRPAAPGIANPEKKNCTGCPNSOS--- 92
DB 29 LPAALAPEDAGEAGADNGAGHRGPHRG---QAEAGAGARDGALHCGPPCPHSDSCIG 84
QY 93 --LSSGPLETKO-NGLWTEAKRDADKMSAREVAISVTENIRQMDRSKR 138
DB 85 RWTSTGTSGHRPCSGGLSVQLLRQMPRSSAEQVRKEIKKIQEORRYR 133

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Search completed: May 20, 2006, 21:23:19
 Job time : 75 secs

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OM protein - protein search, using sw model

Run on: May 20, 2006, 21:23:34 ; Search time 5 Seconds
(without alignments)
61.947 Million cell updates/sec

Title: US-10-705-716a-2

Perfect score: 767
Sequence: 1 MCGGSSRAIDIEPRYSWT.....VTENINQMRSKRYTNCIN 145

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 21570 seqs, 2136119 residues

Total number of hits satisfying chosen parameters: 21570

Minimum DB seq length: 0
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	64.5	8.4	356	US-10-505-928-391	Sequence 391, App
2	64.5	8.4	413	US-10-511-937-2428	Sequence 2428, App
3	64	8.3	262	US-10-370-959-131	Sequence 131, App
4	64	8.3	474	US-11-301-554-1812	Sequence 1812, App
5	63.5	8.3	443	US-10-511-937-2464	Sequence 2464, App
6	62	8.1	2671	US-10-505-928-784	Sequence 784, App
7	61.5	8.0	404	US-11-251-465-23	Sequence 23, App
8	61.5	8.0	1075	US-10-322-936-48	Sequence 48, App
9	60.5	7.9	353	US-10-505-928-851	Sequence 851, App
10	60	7.8	428	US-10-196-749-514	Sequence 514, App
11	59.5	7.8	734	US-10-196-749-458	Sequence 458, App
12	59	7.7	702	US-10-538-066-363	Sequence 363, App
13	59	7.7	2026	US-10-505-928-831	Sequence 831, App
14	58.5	7.6	663	US-11-169-140-14	Sequence 14, App
15	58.5	7.6	4590	US-10-505-928-569	Sequence 569, App
16	58	7.6	564	US-10-511-937-2557	Sequence 2557, App
17	58	7.6	730	US-10-505-928-841	Sequence 841, App
18	58	7.6	1645	US-10-505-928-581	Sequence 581, App
19	58	7.6	2413	US-10-511-937-2616	Sequence 2616, App
20	57.5	7.5	980	US-11-242-505A-36	Sequence 36, App
21	57	7.4	635	US-10-511-937-2424	Sequence 2424, App
22	57	7.4	720	US-10-505-928-383	Sequence 383, App
23	56.5	7.4	400	US-11-183-218-46	Sequence 46, App
24	56.5	7.4	558	US-11-311-754-31	Sequence 31, App
25	56.5	7.4	678	US-10-196-749-150	Sequence 150, App

26	56.5	7.4	678	US-11-101-316-34	Sequence 34, App
27	56.5	7.4	5738	US-10-505-928-150	Sequence 150, App
28	56	7.3	140	US-10-468-193-11	Sequence 11, App
29	56	7.3	341	US-10-196-749-224	Sequence 224, App
30	56	7.3	453	US-10-196-749-64	Sequence 64, App
31	56	7.3	541	US-10-468-193-26	Sequence 26, App
32	56	7.3	3256	US-10-505-928-357	Sequence 357, App
33	55.5	7.2	325	US-10-196-749-238	Sequence 238, App
34	55.5	7.2	325	US-11-101-316-64	Sequence 64, App
35	55.5	7.2	524	US-10-918-905-2	Sequence 2, App
36	55.5	7.2	538	US-11-246-999-138	Sequence 138, App
37	55.5	7.2	919	US-11-251-465-31	Sequence 31, App
38	55	7.2	307	US-11-167-773-51	Sequence 51, App
39	55	7.2	307	US-11-167-773-61	Sequence 61, App
40	55	7.2	307	US-11-167-773-74	Sequence 74, App
41	55	7.2	387	US-10-733-816-6	Sequence 6, App
42	55	7.2	461	US-10-511-937-2945	Sequence 2945, App
43	55	7.2	461	US-11-183-218-32	Sequence 32, App
44	55	7.2	473	US-10-505-928-133	Sequence 133, App
45	55	7.2	483	US-10-733-816-4	Sequence 4, App

ALIGNMENTS

```
RESULT 1
US-10-505-928-391
; Sequence 391, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; PRIOR FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 391
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-505-928-391

Query Match      8.4%; Score 64.5; DB 6; Length 356;
Best Local Similarity 35.8%; Pred. No. 5.1;
Matches 19; Conservative 8; Mismatches 17; Indels 9; Gaps 4;

QY      60 PESNGVLRAPADGAIAPKKNKCTGCPNSOSLSGGP--LTOKONGLTWTTTA 110
DB      225 PDLPGVL-PAPPDG---PEER---GHSPEPSVGBGPGGVTSMPESMMSGQA 270

RESULT 2
US-10-511-937-2428
; Sequence 2428, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; PRIOR FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
```

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; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2428
; LENGTH: 413
; TYPE: PR
; ORGANISM: Homo sapiens
US-10-511-937-2428

Query Match
Best Local Similarity 24.4%; Score 64.5; DB 6; Length 413;
Matches 23; Conservative 12; Mismatches 25; Indels 35; Gaps 4;

63 NGVLRPAAGGIANPEKKN---NCGTQCPNSQSL-----SSG-----96
235 NGGNRP-----LIRPKRLIVSRAGTQCTNTTTTLMRRNAGDPVNCAGLYYKCH 289
97 -----PLTKONGIMTTEAKRDAKMSAREVAISVT 127
290 QVVRPLTKRKGIGTNRKASGKGGKSSLGCT 324

RESULT 3
US-10-370-959-131
; Sequence 131, Application US/10370959
; Publication No. US20060088907A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Williamson, Mark W.
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Macbeth, Kyle J.
; APPLICANT: Hunter, John J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Bandaru, Rajasekhar
; APPLICANT: Tsai, Fong-Ying
; TITLE OF INVENTION: NOVEL 13237, 18480, 2245, 16228, 7677,
; TITLE OF INVENTION: 26320, 46619, 33166, 16836, 46867, 21617, 55562, 39228,
; TITLE OF INVENTION: 62088, 46745, 23155, 21657, 42755, 32229, 22325, 46863, AND
; TITLE OF INVENTION: 32252 MOLECULES AND USES THEREFOR
; FILE REFERENCES: MP103-0170KNMIM
; CURRENT APPLICATION NUMBER: US/10/370,959
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 09/910,150
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/219,028
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: US 10/251,507
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 09/715,479
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 60/218,053
; PRIOR FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: US 09/644,929
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: US 60/212,439
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 09/892,870
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,174
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 09/775,117
; PRIOR FILING DATE: 2001-02-01
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 131
; LENGTH: 262
; TYPE: PR
```

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus amino acid sequence
US-10-370-959-131

Query Match
Best Local Similarity 24.7%; Score 64; DB 6; Length 262;
Matches 20; Conservative 9; Mismatches 32; Indels 20; Gaps 2;

70 APGCIANP-----EKKN-----NCGTQCPNSQSLSSGPTLKONGIMTTR 109
95 APBARGNPQVLYEKSLGPKHIEGYVLDAHGNCTILGNRBCSGDQKGINRTQKSIETVAPSQ 154
110 ARDARMSAREVAISVTENT 130
155 TLTDERQMLREAAVIAHNV 175

RESULT 4
US-11-301-554-1812
; Sequence 1812, Application US/11301554
; Publication No. US20060088527A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvyck, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C21
; CURRENT APPLICATION NUMBER: US/11/301,554
; PRIOR FILING DATE: 2005-12-13
; PRIOR APPLICATION NUMBER: US 10/283,017
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US 10/113,872
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 10/017,754
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 09/902,941
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 09/849,626
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 09/736,457
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 09/702,705
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/677,419
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/671,325
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/658,824
; PRIOR FILING DATE: 2000-09-08
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1812
; LENGTH: 474
; TYPE: PR
; ORGANISM: Homo sapiens
US-11-301-554-1812

Query Match
Best Local Similarity 24.5%; Score 64; DB 7; Length 474;
Matches 26; Conservative 7; Mismatches 27; Indels 46; Gaps 3;
```


Qy 27 WLITDSDALP-----SAAITDSCP----- 46
Db 97 WKLKDSKIPFIREAEFLRLKHMADYDYKTRPKRYKSGNANSSSAAASKEGKGD 156
Qy 47 -----EAGGIHAGVLEDGPPSSNGVLRPAAPGIAN--PEKKNCGTO 86
Db 157 KVGSGGGGGHGGGGGGSSNAGGGGGGAGSGGANSKPAQKSCSK 202

RESULT 5

US-10-511-937-2464
; Sequence 2464, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 50661200104
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: US/10/511,937
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2464
; LENGTH: 443
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2464

Query Match 8.3%; Score 63.5; DB 6; Length 443;
Best Local Similarity 20.8%; Pred. No. 8.9;
Matches 20; Conservative 16; Mismatches 25; Indels 35; Gaps 3;

Qy 63 NGVLRPAAPGIANPEKKM-----CGTQCPNSOSLS----- 94
Db 294 NGQRRP-----LTFPKRLSHARRAGTSCANCOTTITTLWFRNANGDPVCNACGLYTKLH 348
Qy 95 --SGPLTOKONGLWTTTEAKRDAKMSAREVAISYTE 128
Db 349 NINRPLTMKEGIGTRNRKMSKSKCKKVDLSLED 384

RESULT 6

US-10-505-928-784
; Sequence 784, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 784
; LENGTH: 2671
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-505-928-784

Query Match 8.1%; Score 62; DB 6; Length 2671;
Best Local Similarity 29.3%; Pred. No. 1.5e+02;
Matches 27; Conservative 16; Mismatches 33; Indels 16; Gaps 7;

Qy 54 GVLEDESSNGVLRPAAPGIANPEKKM-NGTQ-CF-NSQSLSGPTLQKNGLWTTTEA 110
Db 30 GLVDD---RCVFPAA-GGLDNPKKPRDCLFVYCPNRYIS-----AQKQ--YWKAKQ 76
Qy 111 KRDAKMSAREVAISVTENIRQMDRSKRYTKN 142
Db 77 TKQDKKIALDVVLQKQLQHAQMEKQNDTEN 108

RESULT 7

US-11-251-465-23
; Sequence 23, Application US/11251465
; Publication No. US20060094061A1
; GENERAL INFORMATION:
; APPLICANT: Brys, Reginald
; APPLICANT: Vandeghinste, Nick
; APPLICANT: Tomme, Peter
; APPLICANT: Klaassen, Hubertus
; TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
; TITLE OF INVENTION: Same, Useful In The Treatment Of Joint Degenerative And
; FILE REFERENCE: P30, 172-A USA
; CURRENT APPLICATION NUMBER: US/11/251,465
; CURRENT FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: 60/619,384
; PRIOR FILING DATE: 2004-10-15
; NUMBER OF SEQ ID NOS: 880
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-251-465-23

Query Match 8.0%; Score 61.5; DB 7; Length 404;
Best Local Similarity 28.6%; Pred. No. 13;
Matches 28; Conservative 11; Mismatches 42; Indels 17; Gaps 5;

Qy 42 TDSGPEXGIIHAGVLEDGPPSSNGVLRPAAPGIANPEKKMCGTQCPNSOSLSGPTLQK 101
Db 15 TNGVDKAGGYPRRAEDDSAPPGAASDAERGPGLQVDC--VVGCDK---SSG-----K 66
Qy 102 QNGLWTTT-AKRDAKMSAREVAISVTENIRQMDRSKR 138
Db 67 HGVFTCEGCKSPFKR-----SIRRLSYTCRSNR 96

RESULT 8

US-10-322-836-48
; Sequence 48, Application US/10322836
; Publication No. US20060090212A1
; GENERAL INFORMATION:
; APPLICANT: Turner, Alexander C., Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Freidrich, Glenn A.
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND PROTEINS
; TITLE OF INVENTION: ENCODED THEREBY
; FILE REFERENCE: 8535-0037-999
; CURRENT APPLICATION NUMBER: US/10/322,836
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: US/09/579,114
; PRIOR FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatSeq for Windows Version 3.0
; SEQ ID NO 48

LENGTH: 1075
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (130)...(130)
OTHER INFORMATION: Xaa = Gln or STOP
FEATURE:
NAME/KEY: SITE
LOCATION: (179)...(179)
OTHER INFORMATION: Xaa = Ser or Gly
US-10-322-836-48

Query Match 8.0%; Score 61.5; DB 6; Length 1075;
Best Local Similarity 23.9%; Pred. No. 49;
Matches 27; Conservative 15; Mismatches 52; Indels 19; Gaps 3;

Qy 34 DALPSAATSGPEAGGLHAGVLEDDGSSNGVLRPAAPGIANPEKKNCGTCPCNSQSL 93
Db 860 DTPPRAACSSPHKIPITRGRIE-SPEKRMATFGSAGSINYPDKK-----AL 907

Qy 94 SSGPLTKQNGLTTEAKRDARSAAREVAISYTE-----NIRQDRSKRV 139
Db 908 SEGHSMRSTGSTRHSLGPHKSLAEALADIEKTMSTALHELRERQTV 960

RESULT 9

US-10-505-928-851
Sequence 851, Application US/10505928
Publication No. US20060088532A1
GENERAL INFORMATION:
APPLICANT: Ludwig Institute for Cancer Research et al.
TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
FILE REFERENCE: 28967/39178
CURRENT APPLICATION NUMBER: US/10/505,928
CURRENT FILING DATE: 2004-08-27
PRIOR APPLICATION NUMBER: US 60/363,019
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 866
SOFTWARE: PatentIn 3.2
SEQ ID NO 851
LENGTH: 353
TYPE: PRT
ORGANISM: Homo sapiens
US-10-505-928-851

Query Match 7.9%; Score 60.5; DB 6; Length 353;
Best Local Similarity 29.1%; Pred. No. 14;
Matches 25; Conservative 12; Mismatches 32; Indels 17; Gaps 4;

Qy 37 PSAAATSGPEAGGLHAGVLEDDGSSNGVLRPAAPGIA--NPEKKNCG 83
Db 8 PSEHHEARPRAG---AMSTFAGSRDSRAMPDAGNHTLAQTASPDTEFGHSGCNKA 64

Qy 84 GTCCPNSQSLSGGLTKQNGLWTE 109
Db 65 GVSTPTGSMCP-FOQAQEVGPWTTE 89

RESULT 10
US-10-196-749-514
Sequence 514, Application US/10196749
Publication No. US20060094864A1
GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C340
CURRENT APPLICATION NUMBER: US/10/196,749
CURRENT FILING DATE: 2002-07-16
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 514
LENGTH: 428
TYPE: PRT
ORGANISM: Homo sapiens
US-10-196-749-514

Query Match 7.8%; Score 60; DB 6; Length 428;
Best Local Similarity 19.3%; Pred. No. 20;
Matches 31; Conservative 29; Mismatches 79; Indels 22; Gaps 4;

Qy 2 GCCGSRADAIPRYYSWTRETESTWL-TYTDALPSAATDSGPEAGGLHAGVLEDDG 60
Db 87 GRPLOTDLHAGSRERHRYGTQTSWTSSCTRNMAISSYSS-----TGLGLKKRRGP 141

Qy 61 SSNG--VLRPAAPGIANPEKKNCGTCPCNSQSLSSGGLTKQNGLTTEAKRDKR- 116
Db 142 ASHCQLTSSKTSVEDRPAVSGHTQCEKADIAPOQTILRLNDSSTSEASRSTHK 201

Qy 117 -----MSAREVAISVTENIRQMDRSRYTKNCIN 145
Db 202 FPLPRRGRGEPMLPPLELGYRVTVEDLDREKAAFORIN 242

RESULT 11

US-10-196-749-458
Sequence 458, Application US/10196749
Publication No. US20060094864A1
GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C340
CURRENT APPLICATION NUMBER: US/10/196,749
CURRENT FILING DATE: 2002-07-16

PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 458
LENGTH: 734
TYPE: PRT
ORGANISM: Homo Sapien
US-10-196-749-458

Query Match 7.8%; Score 59.5; DB 6; Length 734;
Best Local Similarity 30.4%; Pred. No. 48;

Matches 24; Conservative 15; Mismatches 27; Indels 13; Gaps 5;

QY 33 SDALPSAATDS---GPEAG--GLHAGVLEDPSSNGVLRPAAGGIANPEKKNCGTQC 87
DB 126 SDSLEASSSFCGLGPHRGLNTHSG-LEDGDLVDGAM--CAEQPADPFWQVDAG--- 179

QY 88 PMSGLSSGPILOKONLIM 106
DB 180 --HPTSPGVITQGRNSVM 196

RESULT 12

US-10-538-066-363
Sequence 363, Application US/10538066
Publication No. US20060094649A1
GENERAL INFORMATION:
APPLICANT: BpImmune Inc.
TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen
FILE REFERENCE: 2060.015PC06
CURRENT APPLICATION NUMBER: US/10/538,066
CURRENT FILING DATE: 2005-06-09
PRIOR APPLICATION NUMBER: US 60/432,017
PRIOR FILING DATE: 2002-12-10
NUMBER OF SEQ ID NOS: 767
SOFTWARE: PatentIn version 3.2
SEQ ID NO 363
LENGTH: 702
TYPE: PRT
ORGANISM: Homo sapiens
US-10-538-066-363

Query Match 7.7%; Score 59; DB 6; Length 702;
Best Local Similarity 18.5%; Pred. No. 51;

Matches 36; Conservative 34; Mismatches 67; Indels 58; Gaps 9;

QY 6 SRDAIEPRYESTRTE---STWLTYYTSDALP-----SAAATDSC 45

DB 330 NNSNPVEDDAVMTCEPIONTYLTWVNNQSLPVSPIRLSNDNRTLLSTTRNDVG 389

QY 46 PEGAGLHAGVLEDP-----GPSNGVLRPA---APG-----GIANPEKKN 82

DB 390 PYECGIQNEISVDSHSDVILANLVKGP--DDPTISPSYTYTRPGVNLSCGAASNPAYIS 448

QY 83 C---GTCCPNSQSLSGPILOKONGLMTTAKDA---KMSAREVAISV-----TE 128
DB 449 WLIDGNIQOHTOEPLFSNITERKNSGLYCOANNSAGSHSTYTVTSABLPSPSSSN 508

QY 129 NIRMDSKRVTKNC 143
DB 509 NSKPEVDKDAVAFTC 523

RESULT 13

US-10-505-928-831
Sequence 831, Application US/10505928
Publication No. US20060088532A1
GENERAL INFORMATION:
APPLICANT: Ludwig Institute for Cancer Research et al.
TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
FILE REFERENCE: 28967/39178
CURRENT APPLICATION NUMBER: US/10/505,928
CURRENT FILING DATE: 2004-08-27
PRIOR APPLICATION NUMBER: US 60/363,019
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 866
SOFTWARE: PatentIn 3.2
SEQ ID NO 831
LENGTH: 2026
TYPE: PRT
ORGANISM: Homo sapiens
US-10-505-928-831

Query Match 7.7%; Score 59; DB 6; Length 2026;
Best Local Similarity 27.8%; Pred. No. 2,2e+02;

Matches 27; Conservative 12; Mismatches 32; Indels 26; Gaps 7;

QY 2 GCGSRADATPRYESTRTEES--TWLTYYTSDALPSAATDSGPEAGGLHAGVLEDP 60
DB 798 GVGLRCDCRCEPFWNFRGIVTDRSGCTPCSD--PQAVRVDCEOMTLC----- 848

QY 61 SNGVLRPAAPGIANPEKKNCGTCCPNSQSLSG 97
DB 849 -----CKP-----GVAGPK-----CG-QCPDGRAL--GP 869

RESULT 14

US-11-169-140-14
Sequence 14, Application US/11169140
Publication No. US20060099150A1
GENERAL INFORMATION:
APPLICANT: ARIZONA PHARMACEUTICALS, INC.
APPLICANT: HOUSTON, Lou, L.
APPLICANT: SHERIDAN, Philip, J.
APPLICANT: HAWLEY, Stephen
APPLICANT: GILPIN, Jacqueline, M.
TITLE OF INVENTION: METHODS FOR THE TRANSPORT OF BIOLOGICALLY ACTIVE AGENTS ACROSS
FILE REFERENCE: 11474-037-999
CURRENT APPLICATION NUMBER: US/11/169,140
CURRENT FILING DATE: 2005-06-27
PRIOR APPLICATION NUMBER: US 60/267,601
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/248,819
PRIOR FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 60/248,478
PRIOR FILING DATE: 2000-11-13
PRIOR APPLICATION NUMBER: US 60/237,929
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PRIOR APPLICATION NUMBER: 09/949,039
PRIOR FILING DATE: 2001-09-06
PRIOR APPLICATION NUMBER: 09/969,748
PRIOR FILING DATE: 2001-10-02
NUMBER OF SEQ ID NOS: 143
SOFTWARE: PatentIn version 3.0

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 20, 2006, 21:06:32 ; Search time 38 Seconds

(without alignments)
367.143 Million cell updates/sec

Title: US-10-705-716a-2

Sequence: 1 MGCGSGRADALFPRYSWT.....VTENIRQNDKSKVTKNCIN 145

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 80.*
2: p1r1.*
3: p1r2.*
4: p1r3.*
5: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	92.5	12.1	571	T43456	hypothetical prote
2	92.5	12.1	778	A35970	erythrocyte-bindin
3	88	11.5	365	GNVSSC	genome polypeptid
4	83	10.8	1433	SS4587	CAT8 protein - yea
5	81	10.6	269	T37073	hypothetical prote
6	79.5	10.4	967	S66852	hypothetical prote
7	79.5	10.4	2559	T09144	probable guanine p
8	78.5	10.2	1199	A40670	nuclear envelope p
9	78	10.2	885	T09225	A kinase anchor pr
10	78	10.2	3488	T34418	hypothetical prote
11	76.5	10.0	600	C69899	conserved hypochet
12	76	9.9	645	S19156	serotonin receptor
13	76	9.9	839	E84824	hypothetical prote
14	75.5	9.8	521	T22571	integrase-like pro
15	75.5	9.8	1063	T03743	bifocal protein -
16	75.5	9.8	1122	T47424	hypothetical prote
17	75	9.8	368	TVMSUL	transforming prote
18	75	9.8	521	IS1633	XpOlycomb - Africa
19	74.5	9.7	601	AH0784	probable transpor
20	74.5	9.7	4957	T03455	AKR protein - huma
21	74.5	9.7	5262	T03454	AKR protein - huma
22	74	9.6	260	B38584	tropomycin I - fruit
23	74	9.6	742	T38801	probable phosphati
24	74	9.6	832	T31878	hypothetical prote
25	74	9.6	962	T00262	hypothetical prote
26	73.5	9.6	876	A57988	regulatory protein
27	73.5	9.6	960	T37916	probable heterochr
28	73.5	9.6	1575	S68448	synaptonemin, 170K
29	73	9.5	403	H98327	enantiomer-selecti

30 73 9.5 453 2 AE2955 glutamyl-tRNA amid
31 73 9.5 781 2 T41551 hypothetical prote
32 73 9.5 1274 2 T37193 enamelin matrix pr
33 72.5 9.5 251 2 C75521 cytochrome-related
34 72.5 9.5 284 2 T51172 transcription fact
35 72.5 9.5 435 2 AG1028 preproliferin
36 72.5 9.5 503 2 T35053 preproliferin
37 72.5 9.5 516 2 JB0301 iminilase (EC 3.2.
38 72.5 9.5 1343 2 AF0611 cell division prot
39 72.5 9.5 3623 2 T08618 intrinsic factor-B
40 72.5 9.5 5327 2 T13564 microtubule-associ
41 72 9.4 108 2 T31565 hypothetical prote
42 72 9.4 1038 1 JC5757 DNA-directed DNA p
43 72 9.4 1038 2 T18222 DNA polymerase del
44 72 9.4 1573 2 T50113 3-dehydroquinase s
45 71.5 9.3 381 2 AB3048 8-amino-7-oxononan

ALIGNMENTS

RESULT 1
T43456
hypothetical protein DKFZp434L061.1 - human
C/Species: Homo sapiens (man)
C/Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C/Accession: T43456
R/Pousetka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, December 1999
A/Reference number: Z22516
A/Accession: T43456
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-571 <AAA>
A/Cross-references: UNIPROT:O75175; UNIPARC:UPI000006FEE9; EMBL:AL133647
A/Experimental source: adult testis; clone DKFZp434L061
C/Genetics:
A/Note: DKFZp434L061.1
C/Superfamily: hydroxyproline-rich glycoprotein

Query Match 12.1%; Score 92.5; DB 2; Length 571;
Best Local Similarity 31.9%; Pred. No. 0.92; Matches 30; Conservative 7; Mismatches 32; Indels 25; Gaps 3;

QY 31 TDSDALPSAATDGPBAGSLH-----AGVLEDPGSSNGVLRPAAP-- 71
DB 111 TDSVSGSPAKNSKGVHSHQPSRAVPTTSGPPPAASLSTTFGNNGVPAAPPS 170

QY 72 --GGIANPEKKNCGTQCPSNGLS---SGPLT 99
DB 171 ALPDKASPAASHNSGTPAPVAYQAVAPAPSGPST 204

RESULT 2
A35970
erythrocyte-binding protein - Plasmodium knowlesi
C/Species: Plasmodium knowlesi
C/Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 09-Jul-2004
C/Accession: A35970
R/Adams, J.H.; Hudson, D.B.; Toril, M.; Ward, G.E.; Wellens, T.E.; Aikawa, M.; Miller, Cell 63, 141-153, 1990
A/Title: The Duffy receptor family of plasmodium knowlesi is located within the micron
A/Reference number: A35970; NCID:91004213; PMID:2170017
A/Accession: A35970
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-778 <ADA>
A/Cross-references: UNIPROT:P22545; UNIPARC:UPI000016BPA8; GB:M68518; GB:M37513; NID:GJ
C/Keywords: transmembrane protein

Query Match 12.1%; Score 92.5; DB 2; Length 778;
Best Local Similarity 33.0%; Pred. No. 1.3; Matches 29; Conservative 12; Mismatches 44; Indels 3; Gaps 3;

QY 31 TDSALPAAATDSGPAGGLHAGVLEDESSNGV-LRPAAPGIANPEKKNAC-GTQCP 88
 DB 352 TVSSDVSIVSGKSGPSTASHALAGNGEVNHTDTEPEKDEKADPOKIDIVKQKDT 411
 QY 89 NSQSLS-GLPTOKNGLMTTEAKRDAD 115
 DB 412 DRSQSGSLGPHTDERTATLGETHMEKDT 439

RESULT 3

GNVSSC

genome polyprotein - sugarcane mosaic virus (strain SC) (fragment)
 N:Contains: carboxyl end of nuclear inclusion protein b; coat protein
 C:Species: sugarcane mosaic virus, SCMV
 C>Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
 C/Accession: PH0207
 R/Frenkel, M.J.; Jilka, J.M.; McKern, N.M.; Strike, P.M.; Clark Jr., J.M.; Shukla, D.D.;
 J. Gen. Virol. 72, 237-242, 1991
 A>Title: Unexpected sequence diversity in the amino-terminal ends of the coat proteins c
 A/Reference number: PH0207; PMID:9113116; PMID:1993866
 A/Accession: PH0207
 A/Molecule type: genomic RNA
 A/Residues: 1-365 <PRE>
 A/Cross-references: UNIPROT:P25242; UNIPARC:UPI0000131E72; GB:D00948; NID:G222123; P1DN:
 C/Superfamily: tobacco etch virus genome polyprotein
 C/Keywords: coat protein; inclusion protein b (fragment) #status predicted <IPB>
 F:1-52/Product: nuclear inclusion protein b (fragment)
 F:53-365/Product: coat protein #status predicted <COA>

Query Match 11.5%; Score 88; DB 1; Length 365;
 Best Local Similarity 21.6%; Pred. No. 1.4; Matches 30; Conservative 24; Mismatches 79; Indels 6; Gaps 4;
 QY 5 GSPADATPEPYRESWTETSTWLTYSDDALPSAATDSGPAGGLHAGVLEDESS 62
 DB 21 GIREBIE KTFKFAKDLGLEYLEDVND-EVFNAGVVDAGAGGAGNAGTQPPATAAA 78
 QY 63 NGVLRPAAPGIANPEKKNACGTQCPNSQSLSGSLPTOKNGLMTTEAKRDADKMSAREV 122
 DB 79 GGAAGPAPATGAAAPPTQ--GSQLPGCATGGGAGTGAAGTGTGGRDQVDAGTT 136
 QY 123 AISTVENIRQMDRSKRTX 141
 DB 137 GKITVPKDKAMSKMRDPK 155

RESULT 4

S54587

CAR8 protein - yeast (Saccharomyces cerevisiae)
 N/Alternate names: MSP8 protein; protein YMR021.06c; protein YMR280C
 C/Species: Saccharomyces cerevisiae
 C>Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 05-Oct-2004
 C/Accession: S54587; S48234; S61595; S49498
 R/Pearson, D.; Bowman, S.
 submitted to the EMBL Data Library, May 1995
 A/Reference number: S54582
 A/Accession: S54587
 A/Molecule type: DNA
 A/Residues: 1-1433 <PEA>
 A/Cross-references: UNIPROT:P31113; UNIPARC:UPI0000127044; EMBL:Z49704; NID:G825540; P1D:
 R/Grzeslitz, D.
 submitted to the EMBL Data Library, March 1994
 A/Reference number: S48234
 A/Accession: S48234
 A/Molecule type: DNA
 A/Residues: 1-746; 'L', 748-1433 <GRZ>
 A/Cross-references: UNIPARC:UPI0000166B45; EMBL:X76344; NID:G559523; P1DN:CAA55139.1; P1:
 R/Boles, B.; Heltmann, C.; Zimmermann, F.K.
 submitted to the EMBL Data Library, December 1995
 A/Reference number: S61594
 A/Accession: S61595

A/Molecule type: DNA
 A/Residues: 1-302; 'A', 304-767; 'A', 769-998; 1003-1007; 'S', 1009-1015; 'Q', 1017-1018; 'P', 102
 A/Cross-references: UNIPARC:UPI0000168D0C; EMBL:X34215; NID:G1122900; P1DN:CAA63906.1;
 A/Experimental source: strain ENY.WA-1A
 C/Genetics:

A/Genes: SGD:CAT8; MSP8
 A/Cross-references: SGD:S0004893; MIPS:YMR280C
 A/Map position: 13R
 C/Keywords: transmembrane protein
 F:65-102/Domain: GAL4 zinc binuclear cluster homology <GAL4>
 F:456-472/Domain: transmembrane #status predicted <TM1>
 F:738-754/Domain: transmembrane #status predicted <TM2>

Query Match 10.8%; Score 83; DB 2; Length 1433;
 Best Local Similarity 29.4%; Pred. No. 20; Matches 32; Conservative 15; Mismatches 50; Indels 12; Gaps 4;
 QY 36 LPAAATDSGPAGGLHAGVLEDESSNGVLRPAAPGIANPEKKNACGTQCPNSQSLS 95
 DB 927 LPATTTSKLPFGSGSKSLERKQRTPVYK-----ENPEHEVLYGDSNNNNSEA 979
 QY 96 G-PLTOKNGLMTTEAKRDADKMSAREVAISTENIR--QMDRSKRT 140
 DB 980 GSPMTNTTNGNRLTYEKDAKR-NKDGISKGEVAHNFQNDTKQMS 1027

RESULT 5

T37073

hypothetical protein SCJ30.06c - Streptomyces coelicolor
 C/Species: Streptomyces coelicolor
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C/Accession: T37073
 R/Sanders, D.C.; Harrie, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.
 submitted to the EMBL Data Library, August 1999
 A/Reference number: Z21621
 A/Accession: T37073
 A/Status: preliminary; translated from GB/EMBL/DDbj
 A/Molecule type: DNA
 A/Residues: 1-269 <SAN>
 A/Cross-references: UNIPROT:Q9S1Y3; UNIPARC:UPI000006C600; EMBL:AL109973; P1DN:CAB53301
 A/Experimental source: strain A3(2)
 C/Genetics:
 A/Genes: SCODEB:SCJ30.06c

Query Match 10.6%; Score 81; DB 2; Length 269;
 Best Local Similarity 26.8%; Pred. No. 4.5; Matches 26; Conservative 9; Mismatches 38; Indels 24; Gaps 4;
 QY 11 IEPRYESWT-----RETSTWLTYSDDALPSAATDSGPAGGLHAGVLEDCP 60
 DB 176 LPETHVQVVPVNFHCRPRRVLRSGLTTPPTVLPSSGCCSGSGBRTG----- 225
 QY 61 SSGVLRPAAPGIANPEKKNACGTQCPNSQSLS 95
 DB 226 GGGVTTGAGGIV-PGRACRCGRRAAHPTASMS 260

RESULT 6

S66852

hypothetical protein YOL155C - yeast (Saccharomyces cerevisiae)
 N/Alternate names: hypothetical protein O0419; protein MOF1001
 C/Species: Saccharomyces cerevisiae
 C>Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 09-Jul-2004
 C/Accession: S66852; S66854; S67325; S70380
 R/Arino, J.; Casamayor, A.; Gamo, F.J.; Gancedo, C.; Lafuente, M.J.; Aldea, M.; Casas,
 submitted to the Protein Sequence Database, July 1996
 A/Reference number: S66814
 A/Accession: S66852
 A/Molecule type: DNA
 A/Residues: 1-967 <RI>
 A/Cross-references: UNIPROT:Q08294; UNIPARC:UPI000006C5C2; EMBL:Z74897; NID:G1420063; F
 A/Experimental source: strain S288C
 R/Gallon, L.; Dujon, B.

submitted to the Protein Sequence Database, July 1996
A/Reference number: S66854
A/Accession: S66854
A/Molecule type: DNA
A/Residues: 1-967 <GAI>
A/Cross-references: UNIPARC:UPI000006C5C2; EMBL:Z74897; NID:g1420063; PID:e251930; PID:g
A/Experimental source: strain S288C
R/Gano, F.J.; Lafuente, M.J.; Casamayor, A.; Aldea, M.; Casas, C.; Arino, J.; Herrero, E.
submitted to the EMBL Data Library, July 1995
A/Description: Analysis of the DNA sequence of a 15500 bp fragment of the left arm of ch
pen reading frames.
A/Reference number: S67324
A/Accession: S67325
A/Molecule type: DNA
A/Residues: 1-164, STSITSGSSSATSSESSVSGSTATSSESSSAGSS', 166-186, 'V', 188-967 <GAM>
A/Cross-references: UNIPARC:UPI000006PEB4; EMBL:X89715; NID:g117620; PID:e190152; PID:g
R/Gano, F.J.; Lafuente, M.J.; Casamayor, A.; Arino, J.; Aldea, M.; Casas, C.; Herrero, E.
Yeast 12, 709-714, 1996
A/Title: Analysis of the DNA sequence of a 15,500 bp fragment near the left telomere of
and two new open reading frames.
A/Reference number: S70379; MUID:96405919; PMID:8810044
A/Accession: S70380
A/Status: nucleic acid sequence not shown
A/Molecule type: DNA
A/Residues: 55-164, 'STSTSGSSSATSSESSVSGSTATSSESSSAGSS', 166-186, 'V', 188-286; 745-773; 781
A/Cross-references: UNIPARC:UPI000017CCC3; UNIPARC:UPI000017CCC4; UNIPARC:UPI000017CCC5;
C/Genetics:
A/Cross-references: SGD:S0005515
A/Map position: 15L
A/Note: YOL155C

Query Match 10.6%; Score 81; DB 2; Length 967;
Best Local Similarity 24.8%; Pred. No. 20;
Matches 29; Conservative 23; Mismatches 55; Indels 10; Gaps 2;

17 ESWTRETSTWLTLYTDSALPSAATDGGPEACG-----LHGVLEDPSSNGVLRPAPG 72
Db 182 ESGSSAGSSSSATSSGSSSVSGSSSATSSESSVSGSSSATSSESSSAGSSSVSSGSSGSS 241
Qy 73 GIANPEKKNCGTQCPNSQSLSSGPLTQKQGLWTTAKRPAKMSAREVAISVTEN 129
Db 242 SSABESSITGGTASGSSASASTSGSVTQSGSSSSAS-----SAGCISSTIDQS 292

RESULT 7
T09144
probable guanine nucleotide exchange factor RhoGEF2 - fruit fly (Drosophila melanogaster)
N/Alternate names: Shar pei/DRhoGEF2
C/Species: Drosophila melanogaster
C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C/Accession: T09144; T09223
R/Haecker, U.; Perrimon, N.
submitted to the EMBL Data Library, October 1997
A/Reference number: Z16586
A/Accession: T09144
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-2559 <HAE>
A/Cross-references: UNIPROT:O44113; UNIPARC:UPI000007F684; EMBL:AF031930; NID:g2687355;
R/Barrett, K.; Leptin, M.; Settleman, J.
Cell 91, 905-915, 1997
A/Title: The Rho GTPase and a putative RhoGEF mediate a signaling pathway for the cell
A/Reference number: Z16618; MUID:98088790; PMID:9428514
A/Accession: T09223
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-676, 'L', 678-837, 'L', 839-889, 'S', 891-1243, 'D', 1245-1358, 'E', 1360-1368, 'R', 1
A/Cross-references: UNIPARC:UPI000007D45E; EMBL:AF032870; NID:g2760367; PIDN:AAC38820.1;
C/Genetics:
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Reference number: Z16620; MUID:98165844; PMID:9497389
A/Accession: T09225
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-885 <DON>
A/Cross-references: UNIPROT:O54931; UNIPARC:UPI0000028356; EMBL:AF033274; NID:g2852696;
A/Note: binds the regulatory subunits (RII) of protein kinase AII isoforms
A/Accession: T09226
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-848, 862-885 <DO2>

C/Function: mediates actin rearrangements required for cell shape changes during ga
C/Suprafamily: rat Munc13-3 protein; protein kinase C zinc-binding repeat homology
C/Keywords: embryo; GTP exchange; signal transduction
F,1151-1200/Domain: protein kinase C zinc-binding repeat homology <KAN>

Query Match 10.4%; Score 79.5; DB 2; Length 2559;
Best Local Similarity 28.3%; Pred. No. 83;
Matches 30; Conservative 11; Mismatches 56; Indels 9; Gaps 3;

5 GSRADATPRYBSWTRETSTWLTLYTDSALPSAATDGPBAGLHAGVLEDPSSNG 64
Db 799 GSSPDNMPKRPDPITKTSSG--EYVKDSESSPPGTPPPYSSSMATVLEDPENNR 857
Qy 65 VLRPAPG-GIANPEKKNCGTQCPNSQSLSSGPL-----TQKQ 102
Db 858 GAAAGCGVFIEHSQFTPMAGASSPPIFSLSHNMMAAQSNDTQGR 903

RESULT 8
A40670
nuclear envelope protein POM 121 - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C/Accession: A40670
R/Hallberg, E.; Wozniak, R.W.; Blobel, G.
J. Cell Biol. 122, 513-521, 1993
A/Title: An integral membrane protein of the pore membrane domain of the nuclear envel
A/Reference number: A40670; MUID:93328754; PMID:8335683
A/Accession: A40670
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1199 <HAL>
A/Cross-references: UNIPROT:P52591; UNIPARC:UPI000012FC0E; GB:Z21513; NID:G396746; PID
F,803-807,845-849,956-960,1010-1014,1047-1051,1076-1080/Region: pentapeptide motif (X-1

Query Match 10.2%; Score 78.5; DB 2; Length 1199;
Best Local Similarity 25.2%; Pred. No. 43;
Matches 39; Conservative 19; Mismatches 56; Indels 41; Gaps 6;

20 TRETBSTWLTLYTDSALPSA---AATDGPBAGLHAGVLEDPSSNGVLRPAPG 75
Db 363 SRTSVSLSLTCTGGLPSSSRNALITSSYSTKVSQLMKRGSTSPSSPASRSQTP 422
Qy 76 -NPEKKNCGTQCPNSQSLSSGPL-----TQKQGLWTT-----EAK 111
Db 423 ERPAKTR--EBRCHQSSSAPLVTKESPGEKVTDPATGKQSLWTSPTPSSSGCRK 480
Qy 112 RDAKMSAR-----EVAISVTENIRQDR 135
Db 481 RKIQLLPSRRGDDQLTPPELGYSTPAEDLDMER 515

RESULT 9
T09225
A kinase anchor protein AKAP-KL isoform 1 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C/Accession: T09225; T09226; T09227
R/Dong, F.; Feldmeier, M.; Casadevall, A.; Rubin, C.S.
J. Biol. Chem. 273, 6533-6541, 1998
A/Title: Molecular characterization of a cDNA that encodes six isoforms of a novel mur
A/Reference number: Z16620; MUID:98165844; PMID:9497389
A/Accession: T09225
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-885 <DON>
A/Cross-references: UNIPROT:O54931; UNIPARC:UPI0000028356; EMBL:AF033274; NID:g2852696;
A/Note: binds the regulatory subunits (RII) of protein kinase AII isoforms
A/Accession: T09226
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-848, 862-885 <DO2>

Db 489 TTTSERKALSGAGVAVAGVAGSGSGSEBAGTGKKNAGVGLGCVLAIANPHOKL--- 545

QY 85 TQCPNSQSLSSGPTLQKNGMLTTEAKRDARMSAREVAI 124

Db 546 -----AKRRQL-LEAKRE-RKAAQTIAI 566

RESULT 13

884824

hypothetical protein At2g40040 [imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C/Accession: B84824

R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanhaken, S.E.; Umayam, L.; Tallon, L.

euse, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A/Reference number: A84420; MUID:20083487; PMID:10617197

A/Accession: B84824

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-839 <STO>

A/Cross-references: UNIPROT:O04207; UNIPARC:UPI00000AB62E; GB:AE002093; NID:G2088657; P

C/Genetics:

A/Gene: At2g40040

A/Map position: 2

Query Match 9.8%; Score 76; DB 2; Length 839;

Best Local Similarity 23.8%; Pred. No. 48;

Matches 40; Conservative 14; Mismatches 62; Indels 52; Gaps 6;

QY 5 GSRADAIETPRYSWTR---ETESTWLTYYTSDALPSAAA----- 41

Db 338 GSGAGVGF-----WNKKSSTESNGATWSSDRTKSGAAWNSWDKNIETDEPPAWG 392

QY 42 -----TDSGPAGGL---HAGVLEDPSSNGV-----LRPAAPGIANPEK 81

Db 393 SGGKNSSETSGPAAWAMDKKSETEPGAGMGCMGKNSSETELGPAAMGMWDKKSDT 452

QY 82 NCGNQCNSQSLSSGPTLQKNGMLTTEAKRDARMSAREVAISVTEN 129

Db 453 KSGPANGSTDAAMWSSDKNN---SETSDAAMGSRNKKTSIES 496

RESULT 14

S22571

integrase-like protein FE65 - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 31-Dec-1993 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004

C/Accession: S22571; S22572

R/Diullo, A.; Zambrano, N.; Mogavero, A.R.; Ammendola, R.; Cimino, F.; Russo, T.

Nucleic Acids Res. 19, 5269-5274, 1991

A/Title: A rat brain mRNA encoding a transcriptional activator homologous to the DNA bit

A/Reference number: S22571; MUID:92020215; PMID:1923810

A/Accession: S22571

A/Molecule type: mRNA

A/Residues: 1-499 <DU11>

A/Cross-references: UNIPROT:Q99MK3; UNIPARC:UPI0000170BC8; EMBL:X60469; NID:G57559; PIN

A/Accession: S22572

A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 31-318 <DU12>

A/Cross-references: UNIPARC:UPI0000170BC9; EMBL:X60468; NID:G57561; PIN:CAA42998.1; P

A/Note: this sequence was submitted to the EMBL Data Library, July 1991

C/Genetics:

A/Intons: 88/3; 107/3; 135/3; 157/3; 207/3; 250/2; 252/2; 290/3

C/Keywords: transcription regulation

F/42-78/Domain: WW repeat homology <WW1>

Query Match 9.8%; Score 75.5; DB 2; Length 499;

Best Local Similarity 25.6%; Pred. No. 29;

Matches 34; Conservative 17; Mismatches 59; Indels 23; Gaps 5;

QY 13 PRYESWTRFETESTWLTYYTSDALPSAAATDSPEBAGGLHAGVLEDPSSNGVLRPAAPG 72

Db 77 PSQNSFQESQQLTWGTF-----AHQGFEEBGF-----WKDPSERAPMEL----- 118

QY 73 GIAPPEKKNCGTQCNSQSLSSGPTLQKNGMLTTEAKRDARMSAREVA-ISVTENIR 131

Db 119 GLADPEB---GTLPPSAQSLSPFPQEBEENLPORNANPGICPAVRSLGWMTEBEL 174

QY 132 QMDRSKRVTKNCI 144

Db 175 APGRSSVAVNNCI 187

RESULT 15

T03743

bifocal protein - fruit fly (Drosophila melanogaster)

C/Species: Drosophila melanogaster

C/Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004

C/Accession: T03743

R/Bahr, S.M.; Yang, X.Y.; Chia, W.

Mol. Cell. Biol. 17, 5521-5529, 1997

A/Title: The Drosophila bifocal gene encodes a novel protein which colocalizes with act

A/Reference number: Z15048; MUID:97415628; PMID:9271427

A/Accession: T03743

A/Status: preliminary; translated from GB/EMBL/DDB

A/Molecule type: mRNA

A/Residues: 1-1063 <BAH>

A/Cross-references: UNIPROT:O16125; UNIPARC:UPI000017BE7D; EMBL:AF011791; NID:G238667,

C/Genetics:

A/Cross-references: FlyBase:FBgn0014133

A/Note: bifocal

Query Match 9.8%; Score 75.5; DB 2; Length 1063;

Best Local Similarity 20.7%; Pred. No. 70;

Matches 39; Conservative 23; Mismatches 59; Indels 67; Gaps 6;

QY 5 GSRADAIETPRYSWTR---ETESTWLTYYTSDAL-----PSAAAT- 42

Db 83 GA1ADFTPATISTSQKRWIMGSEKSKSISNTNSDSTGGHSAVASLSPDAAT 142

QY 43 -----DSPEBAGGLHAGVLEDPSSNGVLRPAAPG 72

Db 143 NVTVP1PKORSSILNTRSGEREMVRYIILSESGRDELESGOPAGVNSRCGEVETG 202

QY 73 GIAPPEKKNCGTQCNSQSLSSGPTLQKNGMLTTEAKRDARMSAREVAISVTENIR 132

Db 203 TIGSPSSAN---QNNPNNLK---TKCKPGQSVABGRPSALG-----TIVNKS 247

QY 133 MDRSKRVT 140

Db 248 CSKTKSIS 255

Search completed: May 20, 2006, 21:07:20
Job time: 40 secs